

APPLICANT: Heston, Warren D.W.
APPLICANT: Fair, William R.
APPLICANT: Overfell, Quathek
APPLICANT: Pinto, John
TITLE OF INVENTION: PROSTATE-SPECIFIC MEMBRANE ANTIGEN AND USES THEREOF
FILE REFERENCE: 1769/41428-G
CURRENT APPLICATION NUMBER: US/08/705,477E
CURRENT FILING DATE: 1996-08-29
NUMBER OF SEQ ID NOS: 128
SOFTWARE: Patentin version 3.1
SEQ ID NO: 96
LENGTH: 783
TYPE: DNA
ORGANISM: Homo sapiens
US-08-705-477E-96

Query Match 3.0%; Score 59; DB 4; Length 783;
Best Local Similarity 100.0%; Pred. No. 3.2e-16;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 560 AAATCGATGTTCTGAGGATTTTATAGCTTATAGTACAAAAGGAAATTTCT 638

RESULT 12
US-08-832-468-2
Sequence 2, Application US/08832468
Patent No. 5962237
GENERAL INFORMATION:
APPLICANT: Ts'O, Paul O.P.
APPLICANT: Wang, Zheng-Pin
APPLICANT: Lesko, Stephen A.
APPLICANT: Nelson, William G.
APPLICANT: Partin, Alan W.
TITLE OF INVENTION: A METHOD OF ENRICHING RARE CELLS
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Leydig, Voit & Mayer, Ltd.
STREET: 700 Thirteenth St., NW
CITY: Washington
STATE: DC
COUNTRY: US
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/832,468
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60-014929
FILING DATE: 05-APR-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Jay, Jeremy M.
REGISTRATION NUMBER: 33587
REFERENCE/DOCKET NUMBER: 72466
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-737-6770
TELEFAX: 202-737-6776
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 50 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid (synthetic DNA)
US-08-832-468-2

Query Match 2.5%; Score 50; DB 2; Length 50;
Best Local Similarity 100.0%; Pred. No. 2.7e-12;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 AGGTCTAGCAACATATGATGTTGTTGAAAGTTTATGATCAATGTT 50

RESULT 13
US-08-832-468-6
Sequence 6, Application US/08832468
Patent No. 5962237

GENERAL INFORMATION:
APPLICANT: Ts'O, Paul O.P.
APPLICANT: Wang, Zheng-Pin
APPLICANT: Lesko, Stephen A.
APPLICANT: Nelson, William G.
APPLICANT: Partin, Alan W.
TITLE OF INVENTION: A METHOD OF ENRICHING RARE CELLS
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Leydig, Voit & Mayer, Ltd.
STREET: 700 Thirteenth St., NW
CITY: Washington
STATE: DC
COUNTRY: US
ZIP: 20005

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/832,468
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60-014929
FILING DATE: 05-APR-1996
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: Jay, Jeremy M.
REGISTRATION NUMBER: 33587
REFERENCE/DOCKET NUMBER: 72466
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-737-6770
TELEFAX: 202-737-6776

INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 50 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid (synthetic DNA)
US-08-832-468-6

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Best Local Similarity 100.0%; Pred. No. 2.7e-12;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 GTGTTAGGCTAGCAATTCATATGCTCCCTTTGATTTGTGAGATTA 50

RESULT 14
US-08-394-152A-45/C
Sequence 45, Application US/08394152A
Patent No. 5935818
GENERAL INFORMATION:
APPLICANT: Israel, Ron S.
APPLICANT: Heston, Warren D.W.

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: February 17, 2004, 16:54:30 ; Search time 5285 Seconds

(without alignments)
16336.674 Million cell updates/sec

Title: US-09-973-382C-1

Perfect score: 1992

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Searched: 3470272 seqs, 21671516995 residues

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Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysts of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	810	40.7	2061	6	AX403107
3	742	37.2	2558	6	AX376036
4	646	32.4	2253	6	AX467227
5	646	32.4	2253	6	BD224135
6	646	32.4	2472	9	BC025672
7	646	32.4	2518	9	AF176574
8	646	32.4	2653	6	123794
9	646	32.4	2653	6	AX337951
10	646	32.4	2653	6	AX337498
11	646	32.4	2653	6	AX505108
12	646	32.4	2653	6	HUMPSM
13	595	29.9	2253	9	AY101595
14	428	21.5	13788	9	AP003122
15	428	21.5	192648	2	AC024234
16	385	19.3	2387	6	AR338033
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23	215	10.8	187529	9	AC118273
24	215	10.8	246865	2	AC074003
25	201	10.1	573	9	AF254357
26	137	6.9	156255	2	AP002369
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ALIGNMENTS

RESULT 1	AF261715	1992 bp	MRNA	linear	PRI 02-NOV-2000
LOCUS	AF261715				
DEFINITION	Homo sapiens prostate-specific membrane antigen-like protein				
ACCESSION	AF261715				
VERSION	AF261715				
KEYWORDS	AF261715.1	GI:11078563			
SOURCE					
ORGANISM	Homo sapiens (human)				
REFERENCE	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
TITLE	O'Keefe, D.S., Bacich, D.J. and Hesston, W.D.W.				
	Cloning and Characterization of a novel glutamate-preferring				

peptidase that maps to the SCZD11 locus: a candidate gene for Schizophrenia?

JOURNAL REFERENCE AUTHORS TITLE

2 (bases 1 to 1992)
O'Keefe,D.S., Bacich,D.J. and Heston,W.D.W.
Expression Profile of Prostate-Specific Membrane Antigen (PSMA) versus a Prostate-Specific Membrane Antigen-Like Gene in Normal Tissues, Prostate Cancer and Tumor Associated-Vasculature

JOURNAL REFERENCE AUTHORS TITLE

3 (bases 1 to 1992)
O'Keefe,D.S., Bacich,D.J. and Heston,W.D.W.
Submitted (27-APR-2000) Cancer Biology, Cleveland Clinic Foundation, NB 40, 9500 Euclid Avenue, Cleveland, OH 44195, USA
Location/Qualifiers

FEATURES source

1. 1992
/organism="Homo sapiens"
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1. 1992
/gene="PSMAL/GCP III"
527. 1855
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gene CDS

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ORIGIN

Query Match 100.0%; Score 1992; DB 9; Length 1992;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1992; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 781 TGTGTTTCAATGAACCTGTAGAGCTTTTGAACCTGAAAAGAAAGGTTGACCTTGA 840
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Qy 1801 TGTTCAGACCTTCAAGTCAGAGGAGCTGACAGACTTTGATGATGATGATGATGATGAT 1860
Db 1801 TGTTCAGACCTTCAAGTCAGAGGAGCTGACAGACTTTGATGATGATGATGATGATGAT 1860
Qy 1861 TTCTTTAGAGACTCTGATGATGATTTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1920
Db 1861 TTCTTTAGAGACTCTGATGATGATTTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1920
Qy 1921 TATTTGATTAATTTTAAATTTGATTTTGAATTTAAAGTTGAATTTATATATATATATAT 1980
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Qy 1981 AAAAAAAAAA 1992
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RESULT 2
AX403107 2061 bp DNA linear PAT 02-SEP-2002
LOCUS Sequence 2 from Patent WO0226984.
DEFINITION AX403107
ACCESSION AX403107.1 GI:21388049
VERSION
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Rhodes, K., Betty, M., Ling, H. P. and An, W.
TITLE Potassium channel interactors and uses therefor
JOURNAL Patent: WO 0226984-A 2 04-APR-2002;
Millennium Pharmaceuticals, Inc. (US)
FEATURES
source 1. .2061
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ORIGIN
Query Match 40.7%; Score 810; DB 6; Length 2061;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 810; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1852 TTACAGACAGACCTTTTATAGGATGATGATGATGATGATGATGATGATGATGATGAT 1911
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Db 1912 GCAGGGAGTCATTTCCAGGAATTTATGATGCTGCTGTTGATTTTGAAGCAAAAGTGAC 1971
Qy 1763 CTTTCCAGGCTCGGGGAGATGTAAGAGACAGATTTCTGTCAGGCTTCACAGTGAC 1822
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RESULT 3
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LOCUS Sequence 103 from Patent WO0168848.
DEFINITION AX376036
ACCESSION AX376036
VERSION AX376036.1 GI:19170410
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Baker, K. P., Chen, J., Deenoyers, J., Goddard, A., Godowski, P. J.,
Guirey, A. L., Pan, J., Smith, V., Watanabe, C. K., Wood, W. I. and
Zhang, Z.
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding
JOURNAL the same
Patent: WO 0168848-A 103 20-SEP-2001;
Genentech, Inc. (US)
FEATURES
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ORIGIN /mol_type="unassigned DNA"
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Query Match 37.2%; Score 742; DB 6; Length 2558;
Best Local Similarity 99.3%; Pred. No. 0;
Matches 1142; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

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Db 931 GAGAGTGTGTCCAGCGTGAATAATCTAAATCTGAATGTGAGAGAGCCCTTACA 990

Qy 410 CCAAGTTACCCAGCAATGAATACGCTTAAAGCTGAATGTCAGAGGCTGTGGCTT 469
Db 991 CCAAGTTACCCAGCAATGAATACGCTTAAAGCTGAATGTCAGAGGCTGTGGCTT 1050

Qy 470 CCAAGTTACCTGTTTCATCCAGTTGATATCTATGATGACAGAGGCTCTAGAAAAATG 529
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Qy 530 GGTGGCTCAGACACACAGATGACGCTGAGAGAGAACTCTCAAGTGTCTTCAATGTT 589
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Qy 590 GGAAGTGTGTCTTCTGAAAACTTTTCTTCACAAAAAATCAAGATGACATCCACTTACC 649
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Qy 650 AATGAAGTGAAGAAATTTCAATGTATGATGATCTCTCAGAGAGAGAGTGAACACAGAC 709
Db 1231 AATGAAGTGAAGAAATTTCAATGTATGATGATCTCTCAGAGAGAGAGTGAACACAGAC 1290

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Db 1351 AGTGAAGCACTGTGTTCTATGAAACCTGTGAGAGCTTTGGAACTGAAAAAGAGAGG 1410

Qy 830 TGAAGACCTGAGAAACAATTTTGTGCAAGCTGGAGTCAAGAGAAATTTGGTCTTCT 889
Db 1411 TGAAGACCTGAGAAACAATTTTGTGCAAGCTGGAGTCAAGAGAAATTTGGTCTTCT 1470

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Qy 1370 TCCATAGTCTCCTTTTATGATGTCAGAGATTAATGCTGATGTTTAAAGATAGCTGAC 1429
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Qy 1430 AAAATCTACA 1439
Db 2011 AAAATCTACA 2020

RESULT 4
AX467227
LOCUS AX467227 2253 bp DNA linear PART 16-JUL-2002

DEFINITION Sequence 1 from Patent WO0234287.
ACCESSION AX467227
VERSION AX467227.1 GI:21900509

KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE
1 Beier, A.M., Gautam, A. and Mouritsen, S.R.
Novel therapeutic vaccine formulations
Patent: WO 0234287-A 1 02-MAY-2002;
Pharmexa A/S (DK)

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Location/Qualifiers
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58..2253
misc_feature
58..2253
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Query Match 32.4%; Score 646; DB 6; Length 2253;
Best Local Similarity 99.2%; Pred. No. 0;
Matches 1096; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 335 GGTGGAATCTTCTGAGAGTGTGTCCAGCGTGAATAATCTTAATCTGAATGTGCA 394
Db 733 GGTGGAATCTTCTGAGAGTGTGTCCAGCGTGAATAATCTTAATCTGAATGTGCA 792

Qy 395 GAGAGCCCTTCAACACAGGTTACCAAGCAATGAATACGCTTAAATGCGAATGCA 454

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Db	853	GAGGCTGTGGTGTCTTCCAAAGTATTCCTGTTCATCCAAATGGATACTATGATGCACGAAG	912
QY	515	CTCCAGAAAAAATGGGTGGCTCAGACCAACAAGATAGCAGCGTGGAGAGAAAGTCTCAAA	574
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QY	575	GTGTCTCTCAATGTTCGAACTTGGCTTCTACGTGAAACTTTTCTTACACAAAAGTCAAGATG	634
Db	973	GTGCTCTCAATGTTCGAACTTGGCTTCTACGTGAAACTTTTCTTACACAAAAGTCAAGATG	1033
QY	635	CACATCCACTCTACCAATGAAGTGCAGAAATTTTACATATGTATAGTACTCTCAGAGCA	694
Db	1033	CACATCCACTCTACCAATGAAGTGCAGAAATTTTACATATGTATAGTACTCTCAGAGCA	1092
QY	695	GCAGTGGAAACAGACAGATATGTCTATTCTGGAGAGGTCAACGGGACTCATGGGTGTTGGT	754
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QY	755	GGTATTGACCTCTCAAGTGGAGACGCTGTGTTCAATGAACCTGTGAGAGCTTTGGAAACA	814
Db	1153	GGTATTGACCTCTCAAGTGGAGACGCTGTGTTCAATGAACCTGTGAGAGCTTTGGAAACA	1213
QY	815	CTGAAAAAGGAAGGGTGGAGACTTGTGAAGAAATAATTTGTTTGCAGCTGGAGATGCAGAA	874
Db	1213	CTGAAAAAGGAAGGGTGGAGACTTGTGAAGAAATAATTTGTTTGCAGCTGGAGATGCAGAA	1272
QY	875	GAATTTGGTCTCTCTGTGTTCTACTAGTGGGACAGAGSATTAATTCAGACTCTTCACAGAG	934
Db	1273	GAATTTGGTCTCTCTGTGTTCTACTAGTGGGACAGAGSATTAATTCAGACTCTTCACAGAG	1333
QY	935	CGTGGCGTGGCTTATATTAATGCTGACTCATCTTATGAAGAACTCACTCTGAGAGTT	994
Db	1333	CGTGGCGTGGCTTATATTAATGCTGACTCATCTTATGAAGAACTCACTCTGAGAGTT	1392
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QY	1115	GAGTTCAATGGCATATCCACAGATAGCAAAATTTGGGATCTGGAAATGATTTTGAAGTGTTC	1177
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QY	1235	AAATTCACCGGCTATCCACTGTATCAACGTGTCTATGAAACAATATGAGTTGGTGGAAAG	1294
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QY	1295	TTTTATGATCCAAATGTTTAAATAATCACTCACTGGGCCACAGGTTCCAGAGAGGATGGTG	1355
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QY	1355	TTTGGAGTAGCAATTTCCATATAGTGTCTCCCTTTGATTTGATGAGATTAATGCTAGTTTTA	1414
Db	1753	TTTGGAGTAGCAATTTCCATATAGTGTCTCCCTTTGATTTGATGAGATTAATGCTAGTTTTA	1812
QY	1415	AGAAAGTATGCTGCACAAATCTTACA 1439	
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RESULT 5
BD224135

LOCUS	BD224135	2253 bp	DNA	linear	PAT 17-JUL-2003
DEFINITION	Novel method for vaccine injection for therapeutic purpose.				
ACCESSION	BD224135				
VERSION	BD224135.1	GI:33033905			
KEYWORDS	JP 2002526419-A/1.				
SOURCE	Homo sapiens	(human)			
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.				
AUTHORS	Steinaa, L., Moultsen, S., Nielsen, K.G., Haaning, J., Leach, D., Dalm, I., Gautam, A., Birk, P. and Karlsson, G.				
TITLE	Novel method for vaccine injection for therapeutic purpose				
JOURNAL	Patent: JP 2002526419-A 1 20-AUG-2002;				
COMMENT	M AND B BIOTECH AS OS Homo sapiens (human) PN JP 2002526419-A/1 PD 20-AUG-2002 PF 05-OCT-1999 JP 2000573386 PR 05-OCT-1998 DK PA 199801261, 20-OCT-1998 US 60/105011 PI LUDILA STEINA, SOREN MOULTSEN, KLAUS GREGORIUS NIELSEN, JESPER PI HAANING, PI DANA LEBCH, IBEN DALUM, ANAND GAUTAM, PETER BIRK, GUNILLA KARLSSON PC A61K39/00, A61K39/39, A61P15/00, A61P35/00, C07K14/47, C07K16/18// PC C12N15/09, PC C12N15/00 CC Human DSM' CC ggt or tgg encoding Gly and Trp, respectively FH Key Location/Qualifiers FT CDS (1)..(2253) FT misc_feature (58)..(2253) FT misc_feature (4)..(6). Location/Qualifiers 1..2253 /organism="Homo sapiens" /mol_type="genomic DNA" /db_xref="taxon:9606"				
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ORIGIN	Query Match 33.4%; Score 646; DB 6; Length 2253; Best Local Similarity 99.2%; Pred. No. 0; Matches 1096; Conservative 0; Mismatches 9; Indels 0; Gaps 0;				
Query	335	GGTTGGAATCTTCCTGAGGTGTGTGCAGCGTGAATAATCTTAATCTGAATGTGCA	394		
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Ds	973	GTTGCTTACATGTTGAGCTGGCTTTATCTGAAAATTTTCTACAAAAAGTCAGATG	1032		
Qy	635	CACATTCACCTTACCAATGAAGTGAAGAGATTTTACATGATAGGTACTTCAAGAGA	694		
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Qy	755	GGATTGACCTTCAGAGTGAAGAGCTGTTTTCATGAAAATGTGAGAGACTTTGGAACA	814		

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Qy	815	CTGAAAAAGAAAGGCTGGAGACCTTAGAAGAACATTTTGTTCGACGCTGGGAATGCAGAA	874
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Qy	1235	AAATTCAGCGGCTATCCACTGTATCAGAGTGTCTATGAAACATATGATTTGGTGGAAAG	1294
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Qy	1355	TTTGAGCTAGCCAAATTCATCAGATGCTCCCTTTTGATTTGATCGAATTAATGCTGTAGTTTA	1414
Db	1753	TTTGAGCTAGCCAAATTCATCAGATGCTCCCTTTTGATTTGATCGAATTAATGCTGTAGTTTA	1812
Qy	1415	AGAAAGTATGCTGCAAAATCTACA	1439
Db	1813	AGAAAGTATGCTGCAAAATCTACA	1837
RESULT 6			
LOCUS	BC025672	2472 bp	mRNA linear PRI 06-OCT-2003
DEFINITION	Homo sapiens folate hydrolase (prostate-specific membrane antigen)		
ACCESSION	1, mRNA (CDNA clone MGC:34488 IMAGE:5202715), complete cds.		
VERSION	BC025672		
KEYWORDS	BC025672.1 GI:19343603		
SOURCE	MGC.		
ORGANISM	Homo sapiens (human)		
REFERENCE	Homo sapiens		
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 2472)		
	Strauberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Datchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldi, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Uedlin, T.B., Toshiyuki, S., Caerini, P., Prange, C., Rata, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McWhan, P.J., McErmann, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Wozniak, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hilyk, S.W., Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettelman, M., Maman, A., Rodriguez, S.,		

TITLE	Sanchez, A., Whitting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.T., Skalska, U., Smailus, D.E., Schnerch, A., Schein, J.E., Jones, S.U. and Marra, M.A.
JOURNAL	Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
MEDLINE	Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
REFERENCE	22388257
AUTHORS	12477932
JOURNAL	2 (Bases 1 to 2472)
REMARK	Strausberg, R.
COMMENT	Direct Submission Submitted (06-MAR-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA NIH-MGC Project URL: http://mgc.nci.nih.gov Contact: MGC help desk Email: gcgaps-remail.nih.gov Tissue Procurement: Life Technologies, Inc. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN) DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC), Gaithersburg, Maryland; Web site: http://www.nisc.nih.gov/ Contact: nisc_mgc@nhgri.nih.gov Ahter, N., Ayala, K., Beckstrom-Sternberg, S.M., Benjamin, B., Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S., Dietrich, N.L., Grante, S., Guan, X., Gupta, J., Haghighi, P., Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Latic, P., Legassey, R., Maduro, Q.L., Masiello, C., Mauck, B., Mastrian, S.D., McCloskey, J.C., McDowell, J., Pearson, R., Statukipop, S., Thomas, P.J., Touchman, J.W., Taurgeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L., Young, A., Zhang, L.-H. and Green, E.D.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNLN at: <http://image.lnl.gov>
Series: IRAK Plate: 49 Row: e Column: 5
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 4758397.

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CDs	160..2319

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ORIGIN

Query Match 32.4%; Score 646; DB 9; Length 2518;
 Best Local Similarity 99.2%; Pred. No. 0;
 Matches 1096; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 335 GGTGGAATCTTCTGGAGGTGTGTCACCGTGGAAATATCTAAATCTGAATGTGCA 394
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 DB 1891 TTTGAGCTAGCCAAATTCATAGTGTCTCCCTTTTGTATGTGAGATTATGCTGTAGTTTAA 1950
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RESULT 8

LOCUS 123794 2653 bp DNA linear PAT 07-OCT-1996
 DEFINITION Sequence 1 from patent US 5538866.
 ACCESSION 123794
 VERSION 123794.1 GI:1603664
 KEYWORDS

SOURCE

ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 2653)
 AUTHORS Israeli, R.S., Heston, W.D.W. and Fair, W.R.
 TITLE Prostate-specific membrane antigen
 JOURNAL Patent: US 5538866-A 1 23-JUL-1996;
 FEATURES Location/Qualifiers

source
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ORIGIN

Query Match 32.4%; Score 646; DB 6; Length 2653;
 Best Local Similarity 99.2%; Pred. No. 0;
 Matches 1096; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 335 GGTGGAATCTTCTGGAGGTGTGTCACCGTGGAAATATCTAAATCTGAATGTGCA 394
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 DB 1054 GGAGACCCCTTCACACAGGTTACCCGCAAAATGAATACCTTATGGCATGTGAATTGCA 1113
 QY 455 GAGGCTGTGTCTTCCAGATATTCCTGTTCACTCAGTGGATATGATGACAGAAAG 514
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Db 2074 AGAAAGTATGCTGACAAATCTTACA 2098

RESULT 9
AR337951
LOCUS AR337951 2653 bp DNA linear PAT 17-AUG-2003
DEFINITION Sequence 1 from patent US 6569432.
ACCESSION AR337951
VERSION AR337951.1 GI:33724620
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE
AUTHORS Unclassified.
TITLES 1 (bases 1 to 2653)
JOURNAL Israeli, R.S., Heston, W.D.W., Fair, R., Querfelli, O. and Pinto, J.
Patent: US 6569432-A 1-27-MAY-2003;
FEATURES
Location/Qualifiers
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ORIGIN
Query Match 32.4%; Score 646; DB 6; Length 2653;
Best Local Similarity 99.2%; Pred. No. 0;
Matches 1096; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 335 GATTGAATCTTCTGAGGAGTGTCTCAGCTGAGAAATCTTAATCTGAATGAGCA 394
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Db 1894 AAATTCAGGGGCTATCCAGTGTATCAAGTGTCTATGATTAACATATGATGTTGGAAAG 1953
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Db 2014 TTTGAGCTAGCCAAATTCATATGCTGCTCTTTGATTTGCAATTAATGCTGATTTTA 2073
Qy 1415 AGAAAGTATGCTGACAAATCTTACA 1439
Db 2074 AGAAAGTATGCTGACAAATCTTACA 2098

RESULT 10
AX337498

LOCUS AX337498 2653 bp DNA linear PAT 09-JAN-2002
 DEFINITION Sequence 8007 from Patent WO0194629.
 ACCESSION AX337498
 VERSION AX337498.1 GI:18128217
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
 AUTHORS Young, P.E., Augustus, M., Carter, K.C., Ebner, R., Endress, G.,
 Horrigan, S., Soppet, D.R. and Weaver, Z.
 TITLE Cancer gene determination and therapeutic screening using signature
 gene sets
 JOURNAL Patent: WO 0194629-A 8007 13-DEC-2001;
 Avalon Pharmaceuticals (US)
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Query Match 32.4%; Score 646; DB 6; Length 2653;
 Best Local Similarity 99.2%; Pred. No. 0;
 Matches 1096; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 335 GGTGGAATTTCTCTGAGAGTGTGTCACCGTGGAAATATCTTAATCTGAAATGTGCA 394
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QY 1355 TTTGAGCTAGCCATTTCCATAGTCTCCTTTTGAATGTCGAGATTAATCTGATGTTTA 1414
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QY 1415 AGAAGTATGTCGACAAATCTACA 1439
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RESULT 11
 AX505108 2653 bp DNA linear PAT 27-SEP-2002
 LOCUS AX505108
 DEFINITION Sequence 1 from Patent WO0240059.
 ACCESSION AX505108
 VERSION AX505108.1 GI:23386415
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
 AUTHORS Mincheff, M.S., Loukinov, D.I. and Zoubak, S.
 TITLE Methods and compositions for inducing cell-mediated immune
 responses
 JOURNAL Patent: WO 0240059-A 1 23-MAY-2002;
 American Foundation for Biological Research Inc. (US) ; Mincheff,
 Milcho S. (US) ; Loukinov, Dmitri I. (US) ; Zoubak, Sergei (US)
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Query Match 32.4%; Score 646; DB 6; Length 2653;

Best Local Similarity 99.2%; Pred. No. 0; Mismatches 9; Indels 0; Gaps 0;

Matches 1096; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 335 GGTGGAATCTTCTGAGAGTGTGTCCAGCGTGAATATCTAAATCTGAATGGTGCA 394
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 DB 1054 GGAAGCCTCTCAGACGAGTTACCCAGCAATGATAGCTTATAGCGCGTGAATGCA 1113
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RESULT 12

HUMPSM

HUMPSM 2653 bp mRNA linear PRI 08-JAN-1995
 DEFINITION Human prostate-specific membrane antigen (PSM) mRNA, complete cds.
 ACCESSION M99487
 VERSION M99487.1 GI:190663
 KEYWORDS prostate-specific membrane antigen.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 2653)
 AUTHORS Israeli, R.S., Powell, C.T., Fair, W.R. and Heston, W.D.
 TITLE Molecular cloning of a complementary DNA encoding a
 prostate-specific membrane antigen
 JOURNAL Cancer Res. 53 (2), 227-230 (1993)
 MEDLINE 93113576
 PUBMED 8417812
 COMMENT Original source text: Homo sapiens (tissue library: LNCap cDNA of
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 AAETLSEVA"

ORIGIN

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Query Match 32.4%; Score 646; DB 9; Length 2653;
 Best Local Similarity 99.2%; Pred. No. 0;
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VERSION AY101595.1 GI:21217742
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE
AUTHORS Ye, C.Z., Zhang, F.L., Zhang, Y.K. and Chen, C.O.
TITLE Cloning and sequencing of Chinese prostate-specific membrane antigen
JOURNAL Mianjixue Zazhi 17 (5), 328-330 (2001)
REFERENCE
AUTHORS Ye, C.Z.
TITLE Direct Submission
JOURNAL Submitted (06-MAY-2002) Department of Urology, Zhongshan Hospital, Medical Center of Fudan University, Fenglin Rd 180, Shanghai 200032, China
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ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS 1 (bases 1 to 192648)
TITLE The sequence of Homo sapiens clone
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 192648)
AUTHORS Waterston, R.H.
TITLE Direct Substitution
JOURNAL Submitted (28-FEB-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
COMMENT On Jun 16, 2000 this sequence version replaced gi:7284696.

----- Genome Center -----
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu/gsc/index.shtml
----- Project Information -----
Center project name: H NH0313102
----- Summary Statistics -----
Sequencing vector: M13, 1008
Sequencing vector: plasmid, 08
Chemistry: Dye-primer ET; 100% of reads
Chemistry: Dye-terminator Big Dye; 0% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 181493 bases at least Q40
Consensus quality: 181864 bases at least Q30
Consensus quality: 186864 bases at least Q20
Insert size: 188000; agarose-fp
Insert size: 190048; sum-of-contigs
Quality coverage: 3.74 in Q20 bases; agarose-fp
Quality coverage: 3.73 in Q20 bases; sum-of-contigs

----- NOTE: This is a 'working draft' sequence. It currently
* consists of 27 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

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* 1414 1513: gap of unknown length
* 1514 2978: contig of 1465 bp in length
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* 3079 4859: contig of 1781 bp in length
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* 6824 9068: contig of 2245 bp in length
* 9069 9169: gap of unknown length
* 9170 11510: contig of 2342 bp in length
* 11511 11610: gap of unknown length
* 11611 15431: contig of 3821 bp in length
* 15432 15531: gap of unknown length
* 15532 18469: contig of 2938 bp in length
* 18470 18569: gap of unknown length
* 18570 22092: contig of 3523 bp in length
* 22093 22192: gap of unknown length
* 22193 25250: contig of 3058 bp in length
* 25251 28352: gap of unknown length
* 28353 28452: contig of 3002 bp in length
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* 31550 31649: gap of unknown length
* 31650 34631: contig of 2982 bp in length
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Best Local Similarity 100.0%; Pred. No. 5,6e-218;
Matches 428; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Search completed: February 17, 2004, 19:37:11
Job time : 5294 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 17, 2004, 16:54:29 ; Search time 513 Seconds
(without alignments)
16495.927 Million cell updates/sec

Title: US-09-973-382C-1
Perfect score: 1992
Sequence: 1 agcaaataccactaccaca.....taaaaaaaaaaaaaaaaaa 1992

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 3373863 seqs, 2124099041 residues

Word size : 0

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

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XX
DT 06-MAR-2001 (first entry)
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DE cDNA encoding a prostate-specific membrane antigen-like protein.
XX
KW Human; prostate specific membrane antigen like protein; cancer;
KW PSMA-like protein; chromosome 11q14.3; schizophrenia;
KW schizophrenia disorder type II locus; ss.
XX
OS Homo sapiens.
XX
FH Key location/Qualifiers
FT CDS 527..1855
FT FT /*tag= a
FT FT /product= "prostate-specific membrane antigen-like protein"
XX
PN M0200061605-A1.
XX
PD 19-OCT-2000.
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PF 07-APR-2000; 2000MO-US009417.
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PR 09-APR-1999; 99US-0128839P.
XX
PA (SLOK) SLOAN KETTERING INST CANCER RES.
XX
PI Heston MDW, O'Keefe DS;
XX
DR WPI: 2000-679461/66.
XX
P-PSDB; AAB19377.
XX
PT New DNA fragment encoding mammalian prostate specific membrane antigen
XX (PSMA) like protein, useful for distinguishing mammalian PSMA gene
XX expression or protein from PSMA-like gene expression or protein.
PS Claim 2; Page 56-57; 75pp; English.
XX
CC The present sequence encodes a human prostate specific membrane antigen
XX (PSMA) like protein. The PSMA-like gene is mapped to chromosome 11q14.3,
CC to the schizophrenia disorder type II locus. Antibodies directed against

CC PSMA-like protein are useful for diagnosing cancers (prostate, bladder, pancreatic, sarcoma, melanoma, lung or kidney) or neurological disorders such as schizophrenia. They may also be used for screening for ligands of CC PSMA-like protein and imaging cells expressing PSMA-like protein
XX

Sequence 1992 BP; 638 A; 352 C; 451 G; 551 T; 0 U; 0 Other;

Query Match 100.0%; Score 1992; DB 3; Length 1992;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1992; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1021 GGTATACAACTTAACAAAAGAGCTGAAAAGCCCTGATGAGGCTTTGAAAGCAATCTCT 1080
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QY 1081 TTATGAAAGTGGACTTAAAAAAGTCTTCCCAAGATTCAGTGGATGCCAGATAG 1140
DB 1081 TTATGAAAGTGGACTTAAAAAAGTCTTCCCAAGATTCAGTGGATGCCAGATAG 1140
QY 1141 CAAATGGAGTCTGAAAATGATTTGAGGTTCTTCCAGACATTTGAATGCTTCAAG 1200
DB 1141 CAAATGGAGTCTGAAAATGATTTGAGGTTCTTCCAGACATTTGAATGCTTCAAG 1200
QY 1201 CAGAGCAGGTTATACAAAATTTGGGAAAACAAATTCAGCGCTATCCACTGATCA 1260
DB 1201 CAGAGCAGGTTATACAAAATTTGGGAAAACAAATTCAGCGCTATCCACTGATCA 1260
QY 1261 CAGTGTCTATGAAACATATGAGTGGTGGAAAAAGTTTATGATCCAAATGTTTAAATATCA 1320
DB 1261 CAGTGTCTATGAAACATATGAGTGGTGGAAAAAGTTTATGATCCAAATGTTTAAATATCA 1320
QY 1321 CCTCAGTGGGCCAGGTTCCAGAGAGGATGGTGTGTTGAGTACCAATTCATGATGCT 1380
DB 1321 CCTCAGTGGGCCAGGTTCCAGAGAGGATGGTGTGTTGAGTACCAATTCATGATGCT 1380
QY 1381 CCCTTTGATGTCAGATTTATGCTGATGTTTAAAGAAATGCTGACAAAATCTACAA 1440
DB 1381 CCCTTTGATGTCAGATTTATGCTGATGTTTAAAGAAATGCTGACAAAATCTACAA 1440
QY 1441 TATTTCTATGAAACATCCACAGAAAATGAAGCATCAATGTTTATCATTTGATTTCACTTTT 1500
DB 1441 TATTTCTATGAAACATCCACAGAAAATGAAGCATCAATGTTTATCATTTGATTTCACTTTT 1500
QY 1501 TTCTGAGTAAAAATTTTACAGAAATGCTTCCAAAGTCCAGAGAGACTCCAGAGCTT 1560
DB 1501 TTCTGAGTAAAAATTTTACAGAAATGCTTCCAAAGTCCAGAGAGACTCCAGAGCTT 1560
QY 1561 TGACAAAAGCAACCCATATTTGTTAAGATGATGATGATCAACTATGTTCTGAAAAG 1620
DB 1561 TGACAAAAGCAACCCATATTTGTTAAGATGATGATGATCAACTATGTTCTGAAAAG 1620
QY 1621 AGCATTTATGATCCATTAGGGTTACAGACAGACTTTTATAGGCATGTCATATGC 1680
DB 1621 AGCATTTATGATCCATTAGGGTTACAGACAGACTTTTATAGGCATGTCATATGC 1680
QY 1681 TCCAGACCCCAACAAGATGACAGGGAGTCAATCCAGGAATTTATGATGCTCTGTT 1740
DB 1681 TCCAGACCCCAACAAGATGACAGGGAGTCAATCCAGGAATTTATGATGCTCTGTT 1740
QY 1741 TGAATTTGAAAGCAAGTGAACCTTCCAAAGCTGGGAGATGTAAGAGACAGATTTTC 1800
DB 1741 TGAATTTGAAAGCAAGTGAACCTTCCAAAGCTGGGAGATGTAAGAGACAGATTTTC 1800
QY 1801 TGTTCAGGCTTCAACGTGACAGGACCTGCAAGACTTTGAGTGAAGTACCTTAAGAGA 1860
DB 1801 TGTTCAGGCTTCAACGTGACAGGACCTGCAAGACTTTGAGTGAAGTACCTTAAGAGA 1860
QY 1861 TTCTTTAGAGACTCTGTATGAAATTTGTGTGATGTCCTCAAGAAATTAATTAAGGGTA 1920
DB 1861 TTCTTTAGAGACTCTGTATGAAATTTGTGTGATGTCCTCAAGAAATTAATTAAGGGTA 1920
QY 1921 TATTTGATTAATTTTAAATTTGATATTTGAAATTAAGTGAATATTAATTAATTAATTA 1980
DB 1921 TATTTGATTAATTTTAAATTTGATATTTGAAATTAAGTGAATATTAATTAATTAATTA 1980
QY 1981 AAAAAAAAAA 1992
DB 1981 AAAAAAAAAA 1992

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RESULT 2
AAD34009
ID AAD34009 standard; cDNA; 2061 BP.
XX
AC AAD34009;
XX
DT 25-JUL-2002 (first entry)
XX
DE Human gene 4 cDNA.
XX
KM Human; gene 4; N-acetylated-gamma-linked-acidic dipeptidase; NAALadase;
KM chromosome 11; drug identification; glutamate peptidase modulator;
KM schizophrenia; therapy; gene; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1..2061
FT /tag=
FT /product= "Human protein having NAALadase like activity"
FT /note= "CDS does not include start and stop codon"
FT /partial
XX
PN MO200226991-A2.
XX
PD 04-APR-2002.
XX
PF 21-SEP-2001; 2001WO-EP010998.
XX
PR 28-SEP-2000; 2000EP-00308551.
XX
PA (ALKU) AKZO NOBEL NV.
PA (MEDR-) MED RES COUNCIL.
PA (UYED-) UNIV EDINBURGH.
XX
PI Sample CAM, Dunbar DR;
XX
DR WPI; 2002-362499/39.
DR P-PSDB; AAE21450.
XX
PT Polypeptide with NAALadase (N-acetylated-gamma-linked-acidic dipeptidase)
PT like activity useful for the identification of new drugs, such as
PT glutamate peptidase modulators, which may be used to treat schizophrenia.
XX
PS Claim 2; Page 15; 15pp; English.
XX
CC The present sequence is human gene 4 cDNA which encodes protein having N-
CC acetylated-gamma-linked-acidic dipeptidase (NAALadase) like activity.
CC Gene 4 is located on chromosome 11. The invention relates to human
CC protein having NAALadase like activity and nucleic acid molecule encoding
CC such protein. Sequences of the invention are used to identify drugs such
CC as glutamate peptidase modulators which may be used to treat
CC schizophrenia
XX
SQ Sequence 2061 BP; 630 A; 391 C; 468 G; 572 T; 0 U; 0 Other;
Query Match 40.7%; Score 810; DB 6; Length 2061;
Best Local Similarity 100.0%; Pred. No. 1.6e-290;
Matches 810; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1043 CTGAAAAGCCCTGATGAAGCTTTGAAGGCAATCTTTATGAAATGGACTAATAAAA 1102
DB 1252 CTGAAAAGCCCTGATGAAGCTTTGAAGGCAATCTTTATGAAATGGACTAATAAAA 1311
QY 1103 AGTCCTTCCCAAGATTCAGTGGCATGCCAGAGTAAGCAAAATGGATCTGAAATGAT 1162
DB 1312 AGTCCTTCCCAAGATTCAGTGGCATGCCAGAGTAAGCAAAATGGATCTGAAATGAT 1371
QY 1163 TTGAGGTGTTCTTCCACAGACTTGAATGCTTTCAGGACAGACGGATTAATAAAT 1222
DB 1372 TTGAGGTGTTCTTCCACAGACTTGAATGCTTTCAGGACAGACGGATTAATAAAT 1431
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QY 1223 TGGAAAACAACAATTACAGGGCTATCCATGATACAGAGTCTTAAGAATATGAG 1282
DB 1432 TGGAAAACAACAATTACAGGGCTATCCATGATACAGAGTCTTAAGAATATGAG 1491
QY 1283 TTGATGAAAAGTTTATGATCCAAATGTTAAATATCATCCTCATGCGCCAGGTTGCA 1342
DB 1492 TTGATGAAAAGTTTATGATCCAAATGTTAAATATCATCCTCATGCGCCAGGTTGCA 1551
QY 1343 GAGAGGATGGTGTGTTGAGCTAGCCAAATCCAAATGAGTCTCCCTTTGATGTCAGATTA 1402
DB 1552 GAGAGGATGGTGTGTTGAGCTAGCCAAATCCAAATGAGTCTCCCTTTGATGTCAGATTA 1611
QY 1403 GCGTGATGTTTAAAGAAAGTATGCTGACAAATATACAAATTTCTATGAAATCCACAG 1462
DB 1612 GCGTGATGTTTAAAGAAAGTATGCTGACAAATATACAAATTTCTATGAAATCCACAG 1671
QY 1463 GAATGAAAGACATACAGTTTATCATTTGATTCACCTTTTCTGACAGTAAATAATTTTACA 1522
DB 1672 GAATGAAAGACATACAGTTTATCATTTGATTCACCTTTTCTGACAGTAAATAATTTTACA 1731
QY 1523 GAAATGCTTCCAAAGTTCCAGCCGAGAGACTTCAGAGACTTTGACAAAGCAACCAATATTG 1582
DB 1732 GAAATGCTTCCAAAGTTCCAGCCGAGAGACTTCAGAGACTTTGACAAAGCAACCAATATTG 1791
QY 1583 TTAAAGATGATGATGATGATCACTCATGTTCTGGAAGAGACATTTATGATTCATTAGGG 1642
DB 1792 TTAAAGATGATGATGATGATCACTCATGTTCTGGAAGAGACATTTATGATTCATTAGGG 1851
QY 1643 TTACGACAGACACCTTTTATAGCATGTCATGTCATGTCACAGAGCCCAACAAGTAT 1702
DB 1852 TTACGACAGACACCTTTTATAGCATGTCATGTCATGTCACAGAGCCCAACAAGTAT 1911
QY 1703 GCAAGGAGTCAATCCAGGAATTTATGATGCTCTGTTGATATGAAAGCAAAAGTGAC 1762
DB 1912 GCAAGGAGTCAATCCAGGAATTTATGATGCTCTGTTGATATGAAAGCAAAAGTGAC 1971
QY 1763 CTTTCCAAGCCCTGGGAGATGTGAAGACAGATTTCTGTCGACCTTCAAGTGCAG 1822
DB 1972 CTTTCCAAGCCCTGGGAGATGTGAAGACAGATTTCTGTCGACCTTCAAGTGCAG 2031
QY 1823 GCAGCTGACAGACTTTGAGTGAAGTACG 1852
DB 2032 GCAGCTGACAGACTTTGAGTGAAGTACG 2061
```

RESULT 3
AAC78599
ID AAC78599 standard; cDNA; 2558 BP.
XX
AC AAC78599;
XX
DT 08-FEB-2001 (first entry)
XX
DE Human PRO739 nucleotide sequence SEQ ID NO:617.
XX
KM Human; secreted protein; transmembrane protein; PRO; EST; cytosolic;
KW expressed sequence tag; detection; cancer; ss.
XX
OS Homo sapiens.
XX
PN MO200053756-A2.
XX
PD 14-SEP-2000.
XX
PF 18-FEB-2000; 2000WO-US004341.
XX
PR 08-MAR-1999; 99WO-US005028.
PR 12-MAR-1999; 99US-0123957P.
PR 29-MAR-1999; 99US-0126773P.
PR 21-APR-1999; 99US-0130232P.
PR 28-APR-1999; 99US-0131445P.
PR 14-MAY-1999; 99US-0134287P.

PR 23-JUN-1999; 99US-0141037P.
 PR 26-JUL-1999; 99US-0145698P.
 PR 29-OCT-1999; 99US-0162506P.
 PR 30-NOV-1999; 99MO-US028313.
 PR 02-DEC-1999; 99MO-US028511.
 PR 02-DEC-1999; 99MO-US028565.
 PR 16-DEC-1999; 99MO-US030095.
 PR 30-DEC-1999; 99MO-US031243.
 PR 30-DEC-1999; 99MO-US031274.
 PR 05-JAN-2000; 2000MO-US000219.
 PR 06-JAN-2000; 2000MO-US000277.
 PR 06-JAN-2000; 2000MO-US000376.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL,
 PI Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerltzen ME,
 PI Goddard A, Godowski PJ, Grimaldi CJ, Gunney AL, Hillan KJ,
 PI Kijavyn IJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA, Shelton DL,
 PI Stewart TA, Tumas D, Williams PM, Wood WI;
 XX WPI, 2000-611443/58.
 DR P-PSDB; AAB4334.
 XX
 PT Novel PRO polypeptides and polynucleotides used in detection methods, to
 PT target bioactive molecules to specific cells, and to modulate cellular
 PT activities.
 XX
 PS Claim 2, Fig 235; 636pp; English.
 XX
 PS AAC78458 to AAC78599 represent polynucleotide and EST (expressed sequence
 CC tag) sequences which encode secreted or transmembrane PRO polypeptides.
 CC The PRO polynucleotides and polypeptides have cytosolic activity. The
 CC polynucleotides and polypeptides can be used for detecting the presence
 CC of PRO polypeptides in samples, for linking bioactive molecules to cells
 CC and for modulating biological activities of cells, using the polypeptides
 CC for specific targeting. The polypeptide targeting can be used to kill the
 CC target cells, e.g. for the treatment of cancers. The polypeptide pairs
 CC provide specific targeting of bioactive molecules to cells. AAC78600 to
 CC AAC78987 represent PCR primers and probes used in the isolation of the
 CC PRO polynucleotide sequences
 CC
 XX
 SQ Sequence 2558 BP; 745 A; 509 C; 623 G; 681 T; 0 U; 0 Other;
 Query Match 37.2%; Score 742; DB 3; Length 2558;
 Best Local Similarity 99.3%; Pred. No. 2.5e-265;
 Matches 1142; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
 QY 290 GACCTGCTGACTACTTGTCTCTGGGGTGAAGTCTATCCAGACGGTTGGAATCTTCT 349
 DB 871 GACCTGCTGACTACTTGTCTCTGGGGTGAAGTCTATCCAGACGGTTGGAATCTTCT 930
 QY 350 GAGGCTGCTGCTGAGCGTGAATATCTTAATCTGAATGCTGAGAGAACCTCTTACA 409
 DB 931 GAGGCTGCTGCTGAGCGTGAATATCTTAATCTGAATGCTGAGAGAACCTCTTACA 990
 QY 410 CCAAGTTACCGAAGAAATGAATACGCTTATAGGATGAATGAGAGGCGTGTGCTT 469
 DB 991 CCAAGTTACCGAAGAAATGAATATGCTTATAGGATGAATGAGAGGCGTGTGCTT 1050
 QY 470 CCAAGTTATCTGTTCACTTCCAGTTGATGATGATGATGATGATGATGATGATGATG 529
 DB 1051 CCAAGTTATCTGTTCACTTCCAGTTGATGATGATGATGATGATGATGATGATGATG 1110
 QY 530 GGTGGCTCAGACACCAAGATGACAGCTGAGAGAGAAAGTCTCAAGTGTCTTCAATGTT 589
 DB 1111 GGTGGCTCAGACACCAAGATGACAGCTGAGAGAGAAAGTCTCAAGTGTCTTCAATGTT 1170
 QY 590 GGAACCTGCTTCTGGAATCTTCTTCAACAAATAATCAAGATGACATCCACTTACC 649
 DB 1171 GGAACCTGCTTCTGGAATCTTCTTCAACAAATAATCAAGATGACATCCACTTACC 1230
 QY 650 AATGAAGTACGAGAAATTTACATGTATGATGATGATGATGATGATGATGATGATGATG 709

DB 1231 AATGAAGTACGAGAAATTTACATGTATGATGATGATGATGATGATGATGATGATGATG 1290
 QY 710 AGATATGATCTTCTGGAAGTCAACCGGACCTATGAGGTGTGTGTGTGTGTGTGTGTGTGT 769
 DB 1291 AGATATGATCTTCTGGAAGTCAACCGGACCTATGAGGTGTGTGTGTGTGTGTGTGTGTGT 1350
 QY 770 AGTGAAGCAGCTGTTTGTTCATGAAACTGTGAGAGCTTGTGAACACTGAAAGAGAGAG 829
 DB 1351 AGTGAAGCAGCTGTTTGTTCATGAAACTGTGAGAGCTTGTGAACACTGAAAGAGAGAG 1410
 QY 830 TGGAGACTGAGAAACAAATTTTGTGCACTGAGAGTGCAGAGAAATTTGTGCTTCTT 889
 DB 1411 TGGAGACTGAGAAACAAATTTTGTGCACTGAGAGTGCAGAGAAATTTGTGCTTCTT 1470
 QY 890 GGTTCATGAGTGGGAGAGAGATTAATTAACATCTTCAAGAGCGTGGCTTAT 949
 DB 1471 GGTTCATGAGTGGGAGAGAGATTAATTAACATCTTCAAGAGCGTGGCTTAT 1530
 QY 950 ATTATGCTGACTCATCTATAGAGAACTACACTGTGAGAGTTGATGTACACCACTG 1009
 DB 1531 ATTATGCTGACTCATCTATAGAGAACTACACTGTGAGAGTTGATGTACACCACTG 1590
 QY 1010 ATGTACAGCTTGTATATACAACTTAACAAAGAGCTGAAAGCCCTGATGAGGCTTTGAA 1069
 DB 1591 ATGTACAGCTTGTATATACAACTTAACAAAGAGCTGAAAGCCCTGATGAGGCTTTGAA 1650
 QY 1070 GGCATATCTCTTTATGAAAGTTGAGACTAAAGATCTTCCCAAGATTCAGTGGCAGT 1129
 DB 1651 GGCATATCTCTTTATGAAAGTTGAGACTAAAGATCTTCCCAAGATTCAGTGGCAGT 1710
 QY 1130 CCAGATATAGCAAAATTTGGATCTGGAATGATTTTGAAGTGTCTTCCAGCACTTGA 1189
 DB 1711 CCAGATATAGCAAAATTTGGATCTGGAATGATTTTGAAGTGTCTTCCAGCACTTGA 1770
 QY 1190 ATTGCTTCAAGCAGACGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1249
 DB 1771 ATTGCTTCAAGCAGACGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1830
 QY 1250 CCACTGATACAGATGCTATGAAACATATGATGATGATGATGATGATGATGATGATGATG 1309
 DB 1831 CCACTGATACAGATGCTATGAAACATATGATGATGATGATGATGATGATGATGATGATG 1890
 QY 1310 TTTAATATCACCTCACTGCTGAGCCAGGTTCCAGAGAGGATGATGATGATGATGATGATG 1369
 DB 1891 TTTAATATCACCTCACTGCTGAGCCAGGTTCCAGAGAGGATGATGATGATGATGATGATG 1950
 QY 1430 AAAATCTACA 1439
 DB 2011 AAAATCTACA 2020
 RESULT 4
 AAS45976
 ID AAS45976 standard; cDNA, 2558 BP.
 XX
 AC AAS45976;
 XX
 DT 18-DEC-2001 (first entry)
 XX
 DE Human DNA encoding PRO polypeptide sequence #52.
 XX
 KW PRO polypeptide; mammal; tumour; cancer; human; cattle; horse; sheep; ss;
 KW dog; cat; pig; goat; rabbit; tumour necrosis factor alpha; TNF-alpha;
 KW blood; chondrocyte cell; cell proliferation; cell differentiation; colon;
 KW adrenal; lung; breast; prostate; rectum; cervix; liver; genetic disorder;
 KW PCR primer.
 XX
 OS Homo sapiens.

XX MO200168848-A2.
 XX 20-SEP-2001.
 XX 28-FEB-2001; 2001WO-US006520.
 XX 01-MAR-2000; 2000WO-US005601.
 XX 02-MAR-2000; 2000WO-US005841.
 XX 03-MAR-2000; 2000US-0187202P.
 XX 06-MAR-2000; 2000US-0186968P.
 XX 14-MAR-2000; 2000US-0189320P.
 XX 14-MAR-2000; 2000US-0189328P.
 XX 15-MAR-2000; 2000WO-US006684.
 XX 21-MAR-2000; 2000US-0190828P.
 XX 21-MAR-2000; 2000US-0191007P.
 XX 21-MAR-2000; 2000US-0191048P.
 XX 21-MAR-2000; 2000US-0191314P.
 XX 28-MAR-2000; 2000US-0192655P.
 XX 29-MAR-2000; 2000US-0193032P.
 XX 29-MAR-2000; 2000US-0193053P.
 XX 30-MAR-2000; 2000WO-US008439.
 XX 04-APR-2000; 2000US-0194449P.
 XX 04-APR-2000; 2000US-0194647P.
 XX 11-APR-2000; 2000US-0195975P.
 XX 11-APR-2000; 2000US-0196000P.
 XX 11-APR-2000; 2000US-0196187P.
 XX 11-APR-2000; 2000US-0196650P.
 XX 11-APR-2000; 2000US-0196820P.
 XX 18-APR-2000; 2000US-0198121P.
 XX 18-APR-2000; 2000US-0198585P.
 XX 25-APR-2000; 2000US-0199397P.
 XX 25-APR-2000; 2000US-0199550P.
 XX 25-APR-2000; 2000US-0199654P.
 XX 03-MAY-2000; 2000US-0201516P.
 XX 17-MAY-2000; 2000WO-US013705.
 XX 22-MAY-2000; 2000WO-US014042.
 XX 30-MAY-2000; 2000WO-US014941.
 XX 02-JUN-2000; 2000WO-US015264.
 XX 05-JUN-2000; 2000US-0209832P.
 XX 28-JUL-2000; 2000WO-US020710.
 XX 22-AUG-2000; 2000US-00644848.
 XX 24-AUG-2000; 2000WO-US023328.
 XX 08-NOV-2000; 2000WO-US030952.
 XX 01-DEC-2000; 2000WO-US032678.
 XX 20-DEC-2000; 2000WO-US034956.
 XX (GETH) GENENTECH INC.
 XX Baker KP, Chen J, Desnoyers L, Goddard A, Godowski PJ, Gurney AL,
 XX Pan J, Smith V, Watanabe CK, Wood WI, Zhang Z;
 XX WPI; 2001-602746/68.
 XX P-PSDB; AAU29075.
 XX Novel nucleic acids encoding PRO polypeptides, used to diagnose the
 XX presence of tumors, such as prostate and breast tumors, in mammals and to
 XX screen for modulators of the compounds.
 XX Claim 2; Fig 103; 774pp; English.
 XX Sequences AAS45925-AAS46231 represent DNA molecules encoding and PCR
 XX primers for PRO polypeptides of the invention. The sequences of the
 XX invention can be used to detect the presence of a tumour in a mammal by
 XX comparing the level of expression of a PRO polypeptide in a test sample
 XX of cells from the animal and a control sample of normal cells, whereby a
 XX higher level of expression in the test sample indicates the presence of a
 XX tumour in the mammal. Mammals include dogs, cats, cattle, horses, sheep,
 XX pigs, goats and rabbits but are preferably human. The polypeptides can be
 XX used to stimulate tumour necrosis factor (TNF) alpha release from human
 XX blood, when contacted with it. A specific polypeptide can be used to
 XX stimulate the proliferation or differentiation of chondrocyte cells. The
 XX PRO proteins can be used to determine the presence of tumours and also

CC susceptibility to tumour development, particularly adrenal, lung, colon,
 CC breast, prostate, rectal, cervical, or liver tumours, in mammalian
 CC subjects. The oligonucleotide probes specific for the PRO nucleic acids
 CC can be used for genetic analysis of individuals with genetic disorders
 XX
 XX Sequence 2558 BP; 745 A; 509 C; 623 G; 681 T; 0 U; 0 Other;

Query Match 37.2%; Score 742; DB 4; Length 2558;
 Best Local Similarity 99.3%; Pred. No. 2,56-265;
 Matches 1142; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 290 GACCTGCTGACTACTTGTGCTCTGGGGGGAATCCATCCAGACGGTTGGAAATCTTCC 349
 Db 871 GACCTGCTGACTACTTGTGCTCTGGGGGGAATCCATCCAGACGGTTGGAAATCTTCC 930
 QY 350 GAGAGTGTGTCCAGCGTGGAAATATCTTAAATCTGAATGTGCAGAGACCTCTCACA 409
 Db 931 GAGAGTGTGTCCAGCGTGGAAATATCTTAAATCTGAATGTGCAGAGACCTCTCACA 990
 QY 410 CCAGATTACCCAGCAATGAATACGCTTATAGCAATGAAATTCAGAGCTGTGGTCTT 469
 Db 991 CCAGATTACCCAGCAATGAATATGCTTATAGCGTGGAAATTCAGAGCTGTGGTCTT 1050
 QY 470 CCAAGTATTCCTGTCATCCAGTTGATGATGACAGAAAGCTCTAGAAAAAATG 529
 Db 1051 CCAAGTATTCCTGTCATCCAGTTGATGATGACAGAAAGCTCTAGAAAAAATG 1110
 QY 530 GGTGGCTCAGACACACACAGATAGCAGCTGGAGAGAAAGTCTCAAGTGTCTCAATGT 589
 Db 1111 GGTGGCTCAGACACACACAGATAGCAGCTGGAGAGAAAGTCTCAAGTGTCTCAATGT 1170
 QY 590 GACCTGCTTACTGGAATCTTTCTACCAAAAAAGTCAAGTGCACATCTCACTTACC 649
 Db 1171 GACCTGCTTACTGGAATCTTTCTACCAAAAAAGTCAAGTGCACATCTCACTTACC 1230
 QY 650 AATGAAGTGCAGAAATTTTAACTGATAGTACTCTCAGAGAGCAGTGAACAGAC 709
 Db 1231 AATGAAGTGCAGAAATTTTAACTGATAGTACTCTCAGAGAGCAGTGAACAGAC 1290
 QY 710 AGATATGTCATCTTGGAGAGTCCCGGAGCTCAGTGGGTGTTGGTATTGAACCTCAG 769
 Db 1291 AGATATGTCATCTTGGAGAGTCCCGGAGCTCAGTGGGTGTTGGTATTGAACCTCAG 1350
 QY 770 AGTGAAGCAGCTGTGTTCATGAATACTGTGAGAGCTTTGGAACTGTAAAAAGAGG 829
 Db 1351 AGTGAAGCAGCTGTGTTCATGAATACTGTGAGAGCTTTGGAACTGTAAAAAGAGG 1410
 QY 830 TGGAGACCTAGAAAGCAATTTTGTTCAGAGCTGGAGATGACAGAAATTTGCTTCTT 889
 Db 1411 TGGAGACCTAGAAAGCAATTTTGTTCAGAGCTGGAGATGACAGAAATTTGCTTCTT 1470
 QY 890 GGTTCCTAGTGGGAGAGATTAATTCAGACTCTCTTCAAGAGCGTGGCTGTAT 949
 Db 1471 GGTTCCTAGTGGGAGAGATTAATTCAGACTCTCTTCAAGAGCGTGGCTGTAT 1530
 QY 950 ATTAATGCTGACTCATCTATAGAAAGAACTTACACTCTGAGAGTTGATTAACCACTG 1009
 Db 1531 ATTAATGCTGACTCATCTATAGAAAGAACTTACACTCTGAGAGTTGATTAACCACTG 1590
 QY 1010 ATGTACAGCTTGGTATACAACTTAACAAAGAGCTGAAAGCCCTGATGAAGCTTTGAA 1069
 Db 1591 ATGTACAGCTTGGTATACAACTTAACAAAGAGCTGAAAGCCCTGATGAAGCTTTGAA 1650
 QY 1070 GGGCAATCTCTTATGAAAGTTGACTAAAGAAAGTCTTCCAGAGTTCAGTGGCATG 1129
 Db 1651 GGGCAATCTCTTATGAAAGTTGACTAAAGAAAGTCTTCCAGAGTTCAGTGGCATG 1710
 QY 1130 CCAGATATAGCAAAATTTGGATCTGGAATGATTTTGAAGTGTCTTCCAGAGCTTGA 1189
 Db 1711 CCAGATATAGCAAAATTTGGATCTGGAATGATTTTGAAGTGTCTTCCAGAGCTTGA 1770
 QY 1190 ATTGCTTCAGGAGACAGGTATTAATAAATTTGGGAACAAACAATTCAGCGGCTAT 1249

Db 1771 ATTGCTTCAGGACGAGACCGGTACTAAAAATTGGGAAACAACAAATTCAGCGGCTAT 1830
QY 1250 CCACGTATCAGAGTGTCTATGAACATATGAGTGGTGGAAAAGTTTATGATCCAAATG 1309
Db 1831 CCACGTATCAGAGTGTCTATGAACATATGAGTGGTGGAAAAGTTTATGATCCAAATG 1890
QY 1310 TTTAAATATCAGCTCCTGTGGCCAGAGTTCGAGAGGAGATGGTGTGTTAGCTAGCCAAAT 1369
Db 1891 TTTAAATATCAGCTCCTGTGGCCAGAGTTCGAGAGGAGATGGTGTGTTAGCTAGCCAAAT 1950
QY 1370 TCCATATGCTGCTCCCTTTTGAATTTGCGAGATTATGCTGTAGTTTAAAGAAATGCTGAC 1429
Db 1951 TCCATATGCTGCTCCCTTTTGAATTTGCGAGATTATGCTGTAGTTTAAAGAAATGCTGAC 2010
QY 1430 AAAATCTACA 1439
Db 2011 AAAATCTACA 2020

RESULT 5
ID ABX78579 standard; cDNA; 2558 BP.
AC ABX78579;
XX 15-APR-2003 (first entry)
DT Human PRO polynucleotide #52.
XX
DE
XX
XX Human; PRO; gene; ss; cytosstatic; tumour; cancer; breast; lung; stomach;
KM liver; dog; cat; cow; horse; sheep; pig; goat; rabbit; ADEPT;
KW antibody-dependent enzyme mediated prodrug therapy.
XX
XX Homo sapiens.
XX
XX US2003027272-A1.
XX
PD 06-FEB-2003.
XX
PF 21-JUN-2002; 2002US-00176492.
XX
XX 18-SEP-1997; 97US-0059263P.
PR 18-SEP-1997; 97US-0059266P.
PR 17-OCT-1997; 97US-0062250P.
PR 21-OCT-1997; 97US-0063486P.
PR 24-OCT-1997; 97US-0063120P.
PR 24-OCT-1997; 97US-0063121P.
PR 28-OCT-1997; 97US-0063540P.
PR 28-OCT-1997; 97US-0063541P.
PR 28-OCT-1997; 97US-0063544P.
PR 28-OCT-1997; 97US-0063564P.
PR 29-OCT-1997; 97US-0063734P.
PR 31-OCT-1997; 97US-0063870P.
PR 31-OCT-1997; 97US-0064103P.
PR 13-NOV-1997; 97US-0065311P.
PR 21-NOV-1997; 97US-0066120P.
PR 24-NOV-1997; 97US-0066466P.
PR 24-NOV-1997; 97US-0066772P.
PR 11-DEC-1997; 97US-0069335P.
PR 12-DEC-1997; 97US-0069425P.
PR 17-DEC-1997; 97US-0069870P.
PR 18-DEC-1997; 97US-0068017P.
PR 10-MAR-1998; 98US-0077450P.
PR 11-MAR-1998; 98US-0077632P.
PR 11-MAR-1998; 98US-0077649P.
PR 20-MAR-1998; 98US-0078886P.
PR 20-MAR-1998; 98US-0078939P.
PR 27-MAR-1998; 98US-0079664P.
PR 27-MAR-1998; 98US-0079786P.
PR 31-MAR-1998; 98US-0080107P.
PR 31-MAR-1998; 98US-0080194P.
PR 01-APR-1998; 98US-0080327P.
PR 01-APR-1998; 98US-0080333P.

PR 08-APR-1998; 98US-0081049P.
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KM chondrocyte proliferation; chondrocyte differentiation; tumour;
KM adrenal tumour; lung tumour; colon tumour; breast tumour;
KM prostate tumour; rectal tumour; cervical tumour; liver tumour; gene; ss.
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DB 2011 AAAATCTACA 2020
RESULT 7
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DT 02-AUG-2003 (first entry)
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KW Human; gene; sf; secreted and transmembrane protein; PRO; TNF-alpha;
KW tumour necrosis factor alpha; chondrocyte cell; tumour; gene therapy;
KW tissue typing.
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XX adrenal tumour; lung; colon; breast; prostate; kidney; rectum; cervix;
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XX antithrombotic; veterinary; gene therapy; gene; ss.
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QY	350	GGAGGTGTGTCCACCGGTGAATATATCTTAATCTGAAATGTGTGACGAGAACCTCTTCACA	409	

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Qy	530	GGTGGCTCAGACCAACAGATAGAGCTGAGAGGAAGTCTCAAAGTCTCAAAATGT	589
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DB 2011 AAAATCTTACA 2020

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DT 09-AUG-2003 (first entry)
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XX Human; gene; 56; secreted and transmembrane protein; PRO; TNF-alpha;
KW tumour necrosis factor alpha; chondrocyte cell; tumour; gene therapy;
XX tissue typing.
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OS Homo sapiens.
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PD
XX 27-FEB-2003.
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PF 27-JUN-2002; 2002US-00184627.
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DT cDNA encoding human PRO polypeptide #52.
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DE Human; PRO polypeptide; secreted and transmembrane protein; tumour;
KW chromosome mapping; gene mapping; cytostatic; gene therapy; gene; ss.
XX Homo sapiens.
XX US2003032113-A1.
PD 13-FEB-2003.
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PF 20-JUN-2002; 2002US-00176911.
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QY	470 CCAAGTATTCCTGTTCATCCAGTTGGATATATATATATATATATATATATATATATATAT					529
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11-AUG-2003 (first entry)				
Novel human secreted and transmembrane protein PRO739 cDNA.				

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DT	11-AUG-2003 (first entry)				
XX					
DE	Novel human secreted and transmembrane protein PRO739 cDNA				

XX Human; gene therapy; tissue typing; tumour; chondrocyte proliferation;
KW chondrocyte differentiation; tumour necrosis factor-alpha release; aa;
KM affinity purification; gene.
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KW liver; drug screening; transgenic animal; genetic analysis;
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Query Match 37.2%; Score 742; DB 7; Length 2558;

Best Local Similarity 99.3%; Pred. No. 2.5e-265; Indels 0; Gaps 0;

Matches 1142; Conservative 0; Mismatches 8;

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QY 530 GGTGGCTCAGACACCAAGATGAGTGTGAGAGAGTCTCAAGTGTCTTCAATGTT 589
DB 1111 GGTGGCTCAGACACCAAGATGAGTGTGAGAGAGTCTCAAGTGTCTTCAATGTT 1170
QY 590 GGAAGTGTGTTTCTGGAATCTTCTTACCAAAAAGTCAAGATGATGATGATGATGATGAT 649
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DB 2011 AAAATCTTACA 2020

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RESULT 14

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ID ACA98192 standard; cDNA; 2558 BP.

ACA98192;

25-JUL-2003 (first entry)

Novel human secreted and transmembrane protein PRO739 cDNA.

Human; secreted and transmembrane protein; PRO; transgenic animal;

knockout; chromosome identification; tissue typing; tumour;

chondrocyte proliferation; chondrocyte differentiation;

tumour necrosis factor-alpha release stimulator; gene; ss.

Homo sapiens.

PN US2003036144-A1.
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PF 01-JUL-2002, 2002US-00187601.
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Query Match 37.2%; Score 742; DB 7; Length 2558;

Best Local Similarity 99.3%; Pred. No. 2.5e-265; Matches 1142; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

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QY 1430 AAAATCTACA 1439
DB 2011 AAAATCTACA 2020

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RESULT 15
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DT 18-JUL-2003 (first entry)
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DE Human secreted/transmembrane protein (PRO) cDNA #52.
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KW Human; ss; gene; secreted protein; transmembrane protein; PRO; tumour;
KW Proliferation; differentiation; chondrocyte cell; TNF-alpha;
KW tumour necrosis factor-alpha; gene therapy.
XX
OS Homo sapiens.
XX
PN US2003036149-A1.
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PD 20-FEB-2003.
XX
PF 02-JUL-2002; 2002US-00187746.

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PR 01-SEP-1998; 98US-0098723P.
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PR 02-SEP-1998; 98US-0098821P.
PR 02-SEP-1998; 98US-0098843P.
PR 09-SEP-1998; 98US-0098602P.
PR 10-SEP-1998; 98US-0099741P.
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ALIGNMENTS

RESULT 1
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Sequence 617, Application US/09978295A
Patent No. US20020156006A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Batou, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Bilen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gottlieb, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gueney, Austin L.
APPLICANT: Hillan, Kenneth J
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Paoni, Nicholas F.
APPLICANT: Pan, James/
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OR INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630P1C1
CURRENT APPLICATION NUMBER: US/09/978, 295A
CURRENT FILING DATE: 2001-10-15
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Sequence 617, Application US/09978697

Patent No. US20020169284A1

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi

APPLICANT: Baker Kevin P.

APPLICANT: Botstein, David

APPLICANT: Desnuyers, Luc

APPLICANT: Eaton, Dan

APPLICANT: Ferrara, Napoleon

APPLICANT: Filvaroff, Ellen

APPLICANT: Fong, Sherman

APPLICANT: Gao, Wei-Qiang

APPLICANT: Gerber, Hanspeter

APPLICANT: Gerritsen, Mary E.

APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.

APPLICANT: Grimaldi, J. Christopher

APPLICANT: Gurney, Austin L.

APPLICANT: Hillan, Kenneth J

APPLICANT: Kijavini, Ivar J.

APPLICANT: Kuo, Sophia S.

APPLICANT: Napier, Mary A.

APPLICANT: Pan, James;

APPLICANT: Paoni, Nicholas P.

APPLICANT: Roy, Margaret Ann

APPLICANT: Shelton, David L.

APPLICANT: Stewart, Timothy A.

APPLICANT: Tumas, Daniel

APPLICANT: Williams, P. Mickey

APPLICANT: Wood, William I.

TITLE OR INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

FILE REFERENCE: P2630PIC27

CURRENT APPLICATION NUMBER: US/09/978,697

CURRENT FILING DATE: 2001-10-16

PRIOR APPLICATION NUMBER: 09/918585

PRIOR FILING DATE: 2001-07-30

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61	PRIOR FILING DATE: 1998-04-08	
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 ; PRIOR APPLICATION NUMBER: 60/085704
 ; PRIOR FILING DATE: 1998-05-15
 ; PRIOR APPLICATION NUMBER: 60/085697

Query Match 37.2%; Score 742; DB 9; Length 2558;
 Best Local Similarity 99.3%; Pred. No. 0;
 Matches 1142; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

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 DB 871 GACCTGCTGACTACTTGTGCTGCGGGTGAAGTCTATCCAGCGGTTGGAATCTTCT 930
 QY 350 GGAAGTGTGTCCAGCGTGAATAATCTTAATCTGAATGTGCGAGGACCTCTCACA 409
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 QY 530 GGTGCTCAGACACCCAGATAGCAGCTGAGAGGAATCTCAAGTGTCTCAATGTT 589
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 DB 1171 GGAAGTGTGTCCAGCGTGAATAATCTTAATCTGAATGTGCGAGGACCTCTCACA 1230
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 DB 1291 AGATATGTCAATCTGAGAGTCAACCGGAGCTCATGGTGTGTTGATTTGACCTCAG 1350
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 QY 1010 AATGAAGTGTGAATCAACCTGAAGAGAGTGAAGAGCTGTAAGAGGCTTTGAA 1069
 DB 1591 AATGAAGTGTGAATCAACCTGAAGAGAGTGAAGAGCTGTAAGAGGCTTTGAA 1650
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 DB 1891 TTTAATATCACTCACTGTGCGCCAGGTTGAGAGAGAGTGTGTTGAGCTAGCCAT 1950
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 QY 1430 AAAATCTACA 1439
 DB 2011 AAAATCTACA 2020

RESULT 3
 US-09-978-192A-617
 ; Sequence 617, Application US/09978192A
 ; Patent No. US2002017553A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ashkenazi, Avi
 ; APPLICANT: Baker Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Denoyers, Luc
 ; APPLICANT: Baton, Dan
 ; APPLICANT: Ferrara, Napoleon
 ; APPLICANT: Filvaroff, Ellen
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gao, Wei-Qiang
 ; APPLICANT: Gerber, Hanspeter
 ; APPLICANT: Gerlitsen, Mary E.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, J. Christopher
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Hillan, Kenneth J.
 ; APPLICANT: Kijavlin, Ivar J.
 ; APPLICANT: Kuo, Sophia S.
 ; APPLICANT: Napier, Mary A.
 ; APPLICANT: Pan, James
 ; APPLICANT: Paoni, Nicholas F.
 ; APPLICANT: Roy, Margaret Ann
 ; APPLICANT: Shelton, David L.
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Williams, P. Mickey
 ; APPLICANT: Wood, William I.
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 ; FILE REFERENCE: P2630PIC9
 ; CURRENT APPLICATION NUMBER: US/09/978, 192A
 ; CURRENT FILING DATE: 2001-10-15
 ; PRIOR APPLICATION NUMBER: 09/918585
 ; PRIOR FILING DATE: 2001-07-30
 ; PRIOR APPLICATION NUMBER: 60/062250
 ; PRIOR FILING DATE: 1997-10-17
 ; PRIOR APPLICATION NUMBER: 60/064249
 ; PRIOR FILING DATE: 1997-11-03
 ; PRIOR APPLICATION NUMBER: 60/065311
 ; PRIOR FILING DATE: 1997-11-13
 ; PRIOR APPLICATION NUMBER: 60/066364

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PRIOR FILING DATE: 1998-05-15
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PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085580
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085573
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085704
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085697

Query Match 37.2%; Score 742; DB 9; Length 2558;
Best Local Similarity 99.3%; Pred. No. 0;
Matches 1142; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

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QY 350 GGAGTGTGTCCAGCGTGAAGTATCTTAATCTGAATGGTGAAGGACCTCTCA 409
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QY 710 AGATATGCTATCTGAGGCTCAGGAGCTCATGGTGTGATTTGACCTCAG 769
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QY 1430 AAATCTACA 1439
DB 2011 AAATCTACA 2020

RESULT 4
US-09-999-832A-617
Sequence 617, Application US/0999832A
Publication No. US20020192706A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Batoni, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Bilem
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerltisen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kijavani, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630P1C63
CURRENT APPLICATION NUMBER: US/09/999, 832A
CURRENT FILING DATE: 2001-10-24
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
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 PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/085704
 PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/085697

Query Match 37.28; Score 742; DB 9; Length 2558;
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RESULT 5
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 Sequence 617, Application US/09978189
 Publication No. US20030004102A1
 GENERAL INFORMATION:
 APPLICANT: Ashkenazi, Avi
 APPLICANT: Baker Kevin P.
 APPLICANT: Botstein, David
 APPLICANT: Desnoyers, Luc
 APPLICANT: Eaton, Dan
 APPLICANT: Ferrara, Napoleon
 APPLICANT: Filvaroff, Ellen
 APPLICANT: Fong, Sherman
 APPLICANT: Geo, Wei-Qiang
 APPLICANT: Gerber, Hanspeter
 APPLICANT: Gerlitsen, Mary E.
 APPLICANT: Goddard, Audrey
 APPLICANT: Godowski, Paul J.
 APPLICANT: Grimaldi, J. Christopher
 APPLICANT: Gurney, Austin L.
 APPLICANT: Hillan, Kenneth J.
 APPLICANT: Kijavlin, Ivar J.
 APPLICANT: Kuo, Sophia S.
 APPLICANT: Nadler, Mary A.
 APPLICANT: Pan, James
 APPLICANT: Paoni, Nicholas F.
 APPLICANT: Roy, Margaret Ann
 APPLICANT: Shelton, David L.
 APPLICANT: Stewart, Timothy A.
 APPLICANT: Tumas, Daniel
 APPLICANT: Williams, P. Mickey
 APPLICANT: Wood, William I.
 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 FILE REFERENCE: P2630P1C7
 CURRENT APPLICATION NUMBER: US/09/978,189
 CURRENT FILING DATE: 2001-10-15
 PRIOR APPLICATION NUMBER: 09/918585
 PRIOR FILING DATE: 2001-07-30
 PRIOR APPLICATION NUMBER: 60/062250
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 PRIOR APPLICATION NUMBER: 60/077649

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PRIOR FILING DATE: 1998-04-21	PRIOR APPLICATION NUMBER: 60/082569
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PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085697

Query Match 37.2%; Score 742; DB 10; Length 2558;
Best Local Similarity 99.3%; Pred. No. 0;
Matches 1142; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

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QY 1430 AAAATCTACA 1439
DB 2011 AAAATCTACA 2020

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RESULT 6
US-09-978-608A-617
Sequence 617, Application US/09978608A
Publication No. US2003045462A1

GENERAL INFORMATION:

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APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvarole, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gertlson, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoli, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Thomas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630P1C22
CURRENT APPLICATION NUMBER: US/09/978, 608A
CURRENT FILING DATE: 2001-10-16
NUMBER OF SEQ ID NOS: 624
Prior Application removed - See File Wrapper or Palm
SEQ ID NO 617
LENGTH: 2558
TYPE: DNA
ORGANISM: Homo Sapien
US-09-978-608A-617

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Query Match 37.2%; Score 742; DB 10; Length 2558;
Best Local Similarity 99.3%; Pred. No. 0;
Matches 1142; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

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RESULT 7

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; Sequence 617, Application US/09978585A
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; APPLICANT: Ashkenazi, Avi
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; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
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; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630P1C15
; CURRENT APPLICATION NUMBER: US/09/978, 585A
; NUMBER OF SEQ ID NOS: 624
; Prior Application removed - See File Wrapper or Palm
; SEQ ID NO 617
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; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-978-585A-617
Query Match 37.2%; Score 742; DB 10; Length 2558;
Best Local Similarity 99.3%; Pred. No. 0;
Matches 1142; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
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Query Match 37.2%; Score 742; DB 10; Length 2558;

Best Local Similarity 99.3%; Pred. No. 0;

Matches 1142; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

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Qy 350 GGAGGTGCTGCTGAGCGTGAATAATCTTAATCTGAATGTCAGAGACCTCTCACA 409
Db 931 GGAGGTGCTGCTGAGCGTGAATAATCTTAATCTGAATGTCAGAGACCTCTCACA 990
Qy 410 CCAGGTTACCCAGCAATAATATGCTTATGAGCATGGAATTGACAGAGCTGTGCTT 469
Db 991 CCAGGTTACCCAGCAATAATATGCTTATGAGCATGGAATTGACAGAGCTGTGCTT 1050
Qy 470 CCAAGTATTCCTGTTATCCAGTGGATCTATGATGCAACAAGCTCTAGAAAAATG 529
Db 1051 CCAAGTATTCCTGTTATCCAGTGGATCTATGATGCAACAAGCTCTAGAAAAATG 1110
Qy 530 GGTGCTCAGCACCACAGATAGCAGTGAAGTCTCAAGTGTCTTACATGTT 589
Db 1111 GGTGCTCAGCACCACAGATAGCAGTGAAGTCTCAAGTGTCTTACATGTT 1170
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Db 1231 AATGAAGTACGAGATTTTACATGATGATGATCTCAGAGAGACAGTGAACGAG 1290
Qy 710 AGATATGATCTTGGAGAGTCAACGGAGCTCATGAGGTGTTGTTGTTATGACCTCAG 769

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Qy 1370 TCCATAGTGTCCCTTTGATGTCGAGTTATGCTGATTTAAGAAAGTATGCTGAC 1429
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Qy 1430 AAAATCTACA 1439
Db 2011 AAAATCTACA 2020

APPLICANT: Kljavin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James J.
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tunes, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630P1C17
CURRENT APPLICATION NUMBER: US/09/978,403A
CURRENT FILING DATE: 2002-03-19
PRIOR APPLICATION NUMBER: 09/918585
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Query Match 37.2%; Score 742; DB 10; Length 2558;
Best Local Similarity 99.3%; Pred. No. 0;
Matches 1142; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 290 GACCTGCTGACTTCTTCTCTGGGGTGAAGTCTTATCCGAGCGTTGGAATCTTCTT 349
DB 871 GACCTGCTGACTTCTTCTCTGGGGTGAAGTCTTATCCGAGCGTTGGAATCTTCTT 930
QY 350 GAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 409
DB 931 GAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 990
QY 410 CCAGGTTACCCAGCAATGATAGCTTTATAGCATGATAGCTGCTGCTGCTGCTGCTT 469
DB 991 CCAGGTTACCCAGCAATGATAGCTTTATAGCATGATAGCTGCTGCTGCTGCTGCTT 1050
QY 470 CCAGGTTACCCAGCAATGATAGCTTTATAGCATGATAGCTGCTGCTGCTGCTGCTT 529
DB 1051 CCAGGTTACCCAGCAATGATAGCTTTATAGCATGATAGCTGCTGCTGCTGCTGCTT 1110
QY 530 GGTGGCTGACCAACCAATAGAGCTGAGAGGAGGCTCAAGTGTCTCAATGTT 589
DB 1111 GGTGGCTGACCAACCAATAGAGCTGAGAGGAGGCTCAAGTGTCTCAATGTT 1170
QY 590 GGAAGCTGCTTACTGGAATCTTCTTACACAAAAGTCAAGATGACATCTTACC 649
DB 1171 GGAAGCTGCTTACTGGAATCTTCTTACACAAAAGTCAAGATGACATCTTACC 1230
QY 650 AATGAAGTACGAGAAATTTACATGTGATAGCTTCTAGAGGACATGAACTGAGC 709
DB 1231 AATGAAGTACGAGAAATTTACATGTGATAGCTTCTAGAGGACATGAACTGAGC 1290
QY 710 AGATATGATCTTGGGAGGCTACCGGGAGCTATGGGCTTTGGTGTATTTAGCTTCA 769
DB 1291 AGATATGATCTTGGGAGGCTACCGGGAGCTATGGGCTTTGGTGTATTTAGCTTCA 1350
QY 770 AGTGAGCAGCTGTGTTCTATGAAACTGTGAGAGCTTTGGAACACTGAAAAAGAGGG 829

Db 1351 AGTGGACAGCTGTTGTCATGAATAATGTGAGGAGCTTTGGAACTGGAAGAGAGG 1410
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Db 1411 TGGAGACCTGAGAAAGAAATTTTGTTCAGAGCTGGAGATGAGAAAGATTTGCTTCTT 1470
Qy 890 GGTTCCTAGTGGGAGAGATTAATTAAGACTCTTCAAGAGCTGGAGCTGGCTTAT 949
Db 1471 GGTTCCTAGTGGGAGAGATTAATTAAGACTCTTCAAGAGCTGGAGCTGGCTTAT 1530
Qy 950 ATTATCTGATCATCTATTAAGAAAGAACTACTGAGAGTTGATGACCACTG 1009
Db 1531 ATTATCTGATCATCTATTAAGAAAGAACTACTGAGAGTTGATGACCACTG 1590
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Db 1591 ATGACAGCTTTGATTAACAACCTTAACAAAGAGCTGAAAGCCCTGATGAAGCTTTGAA 1650
Qy 1070 GGCAGATCTCTTATGAAGTTGAGCTAAAGAAAGCTCCAGAGTTCAAGTGGCATG 1129
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Qy 1130 CCGAGATTAAGCAAAATTTGGATCTGAAATGATTTGAGTGTCTTCAAGCACTTGA 1189
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Db 1831 CCACTGATCAGAGTGTCTATGAAGAAACATATGATGTTGAGAAAGTTTATGATCCATG 1890
Qy 1310 TTTAAATATACCTCAGCTGTGCCCCAGGTTGAGAGAGAGATGTTGTTGAGTAGCCAT 1369
Db 1891 TTTAAATATACCTCAGCTGTGCCCCAGGTTGAGAGAGAGATGTTGTTGAGTAGCCAT 1950
Qy 1370 TCCATAGTGTCTCTTTTATTTGATGTTGAGATTTAGCTTATGAGAAAGTATGCTGAC 1429
Db 1951 TCCATAGTGTCTCTTTTATTTGATGTTGAGATTTAGCTTATGAGAAAGTATGCTGAC 2010
Qy 1430 AAAATCTACA 1439
Db 2011 AAAATCTACA 2020

RESULT 10
US-09-978-564A-617
Sequence 617, Application US/09978564A
Publication No. US2003050241A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerltzen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kijavitt, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James

APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tamas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OR INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE OR INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630P1C25
CURRENT APPLICATION NUMBER: US/09/978,564A
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Query Match 37.2%; Score 742; DB 10; Length 2558;

Best Local Similarity 99.3%; Pred. No. 0; Mismatches 8; Indels 0; Gaps 0;

Matches 1142; Conservative 0;

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DB 871 GACCTGCTGACTACTCTTCTCTGCGGTGAAGTCTTATCCAGACGGTGAATCTTCT 930
QY 350 GGAGGTGTGTCTCAGCGTGAATATCTTAATCTGAATGTGTGACAGAACTCTGCACA 409
DB 931 GGAGGTGTGTCTCAGCGTGAATATCTTAATCTGAATGTGTGACAGAACTCTGCACA 990
QY 410 CCAGTTACCCAGCAATGAATAGCTTATAGCAATGTGACAGAGCTCTAGAAAAATG 469
DB 991 CCAGTTACCCAGCAATGAATAGCTTATAGCGCTGAAATGTGACAGAGCTCTAGAAAAATG 1050
QY 470 CCAGTTATCTGCTTCATCCAGTTGATATCTATGATGACAGAACTCTAGAAAAATG 529
DB 1051 CCAGTTATCTGCTTCATCCAGTTGATATCTATGATGATGACAGAACTCTAGAAAAATG 1110
QY 530 GGTGCTCAGCAACCAAGATGACAGTGAAGAGAACTCTAAAGTGTCTTAATGTT 589
DB 1111 GGTGCTCAGCAACCAAGATGACAGTGAAGAGAACTCTAAAGTGTCTTAATGTT 1170
QY 590 GGACCTGGCTTTACCTGGAATCTTTTACACAAAAGTCAAGATGACATCCACTTACC 649
DB 1171 GGACCTGGCTTTACCTGGAATCTTTTACACAAAAGTCAAGATGACATCCACTTACC 1230
QY 650 AATGAAGTACAGAAATTTACATGTATGATGATCTCAGAGAGACAGTGAACAGAC 709
DB 1231 AATGAAGTACAGAAATTTACATGTATGATGATGATCTCAGAGAGACAGTGAACAGAC 1290
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DB 1291 AGATATGCTATCTGGAAGTCAACCGGAACTCATGCGGTGTGTGTGATATGACCTTACG 1350
QY 770 AGTGAAGAGCTGTGTTCATGAACTGTGAGAGCTTTGGAACATGAAAAAGAGG 829
DB 1351 AGTGAAGAGCTGTGTTCATGAACTGTGAGAGCTTTGGAACATGAAAAAGAGG 1410
QY 830 TGAGAGCTAGAAACAATTTTGTTCAGAGCTGGATGACAGAAATTTGTCTTCTT 889

Db 1411 TGGAGACCTAGAGAGCAATTTTGTGCAAGCTGGAGTGAAGAAATTTGGTCTT 1470
Qy 890 GGTTCATCTAGTGGCAGAGAGATATTCAGACTCTCTCAAGGCGTGGCTTAT 949
Db 1471 GGTTCATCTAGTGGCAGAGAGATATTCAGACTCTCTCAAGGCGTGGCTTAT 1530
Qy 950 ATTATCTGATCATCTATATGAAGAAACTACTCTGAGAGTGAATGACACACTG 1009
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Db 1591 ATGTACAGCTTGTATACAACTTAACAAAGAGCTGAAGAGCTTGAAGGCTTGA 1650
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Qy 1310 TTTAAATATACCTCACTGCTGGCCAGGTTGAGAGAGAGAGTGGTGAAGCAAT 1369
Db 1891 TTTAAATATACCTCACTGCTGGCCAGGTTGAGAGAGAGAGTGGTGAAGCAAT 1950
Qy 1370 TCCATAGTGTCTCTTTTGAATGTGAGATTAATGCTTATTAAGAAAGTATGCTGAC 1429
Db 1951 TCCATAGTGTCTCTTTTGAATGTGAGATTAATGCTTATTAAGAAAGTATGCTGAC 2010
Qy 1430 AAAATCTACA 1439
Db 2011 AAAATCTACA 2020

RESULT 11
US-09-999-833A-617
Sequence 617, Application US/09999833A
Publication No. US20030054405A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerltsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Guiney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Nadier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.

APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630P1C65
CURRENT APPLICATION NUMBER: US/09/999,833A
PRIOR FILING DATE: 2001-10-24
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
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PRIOR APPLICATION NUMBER: 60/085573
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085704
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085697

Query Match 37.2%; Score 742; DB 10; Length 2558;
Best Local Similarity 99.3%; Pred. No. 0;
Matches 1142; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

290 GACCCGCTGACTACTTGTCTCTGGGGTGAAGTCTTATCCAGACGGTGAATCTTCT 349
871 GACCTGCTGACTACTTGTCTCTGGGGTGAAGTCTTATCCAGACGGTGAATCTTCT 930
350 GGAGGTGTGTCTCAGCGTGAATATCTTAACTTGAATGTGTGACAGAACCTCTCACA 409
931 GGAGGTGTGTCTCAGCGTGAATATCTTAACTTGAATGTGTGACAGAACCTCTCACA 990
410 CCAGGTTACCCAGCAATGAATACGTTTATAGCATGGAATGTGACAGAGCTGTGGTCTT 469
991 CCAGGTTACCCAGCAATGAATATGTTATAGCGGTGAATGTGACAGAGCTGTGGTCTT 1050
470 CCAAGTATTCGTTGATCGAGTGAATGATGATGACAGAGAGCTCTAGAAAAATG 529
1051 CCAAGTATTCGTTGATCGAGTGAATGATGATGATGATGATGATGATGATGATGATG 1110
530 GGTGCTCAGCACCCAGATAGCAGTGAAGAGAGAGTCTCAAGTGTCTTCAATGTT 589
1111 GGTGCTCAGCACCCAGATAGCAGTGAAGAGAGAGTCTCAAGTGTCTTCAATGTT 1170
590 GGAACCTGGCTTTTACTGGAACCTTTTACACAAAAAGTCAAGTGAATCCACTTACC 649
1171 GGAACCTGGCTTTTACTGGAACCTTTTACACAAAAAGTCAAGTGAATCCACTTACC 1230
650 AATGAAGTGAAGATTTTACATGTAGTACTCTCAGAGAGACAGTGAACAGAC 709
1231 AATGAAGTGAAGATTTTACATGTAGTACTCTCAGAGAGACAGTGAACAGAC 1290
710 AGATATGTCAATTTGGAAGTCAACCGGACCTCAGTGGTGTGTGATATGACCTCAG 769
1291 AGATATGTCAATTTGGAAGTCAACCGGACCTCAGTGGTGTGTGATATGACCTCAG 1350
770 AGTGAAGCAGCTTTTGTATGAATGTGAAGAGTGTGGAACATGAAAAAGAGAGG 829
1351 AGTGAAGCAGCTTTTGTATGAATGTGAAGAGTGTGGAACATGAAAAAGAGAGG 1410
830 TGGAGACCTAGAGAGCAATTTTGTGCAAGCTGGAGTGAAGAGATTTGTCTTCTT 889
1411 TGGAGACCTAGAGAGCAATTTTGTGCAAGCTGGAGTGAAGAGATTTGTCTTCTT 1470
890 GGTTCCTAGAGTGGAGAGATTAATGACAGCTCTTCAAGAGGCTGGGCTTAT 949

Db 1471 GGTCTACTGAGTGGGAGAGAGAAATCAAGACTCCTTCAAGAGCGTGGCTTAT 1530
Qy 950 ATTAATGCTGACTCTATNAGAAGAACTACCTCGAGAGTTGATGACCACTG 1009
Db 1531 ATTAATGCTGACTCTATNAGAAGAACTACCTCGAGAGTTGATGACCACTG 1590
Qy 1010 ATGTAACAGCTTGTATCAACCTAACAAAGAGCTGAAAGCCCTGATGAAGGCTTTGA 1069
Db 1591 ATGTAACAGCTTGTATCAACCTAACAAAGAGCTGAAAGCCCTGATGAAGGCTTTGA 1650
Qy 1070 GGCAAATCTTTATGAAAGTTGACTAAAGAAAGTCTCCAGAGTTGAGTGGCAGT 1129
Db 1651 GGCAAATCTTTATGAAAGTTGACTAAAGAAAGTCTCCAGAGTTGAGTGGCAGT 1710
Qy 1130 CCCAGGATTAAGCAATTTGGGATCTGGAATGATTTTGAAGTCTTCCAGAGTTGGA 1189
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Qy 1190 ATTGCTTCAGGAGAGAGAGGATATCTAAAGTTGGGAAACAAATTCAGCGGCTAT 1249
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Qy 1250 CCAGTGTATCACAGTGTCTATGAACATATGAGTTGTGAAAGTTTATGATCCATG 1309
Db 1831 CCAGTGTATCACAGTGTCTATGAACATATGAGTTGTGAAAGTTTATGATCCATG 1890
Qy 1310 TTTAAATATCACTCAGCTGTGAGGAGTTGAGAGAGGAGTGTGTTGAGCTAGCCAT 1359
Db 1891 TTTAAATATCACTCAGCTGTGAGGAGTTGAGAGAGGAGTGTGTTGAGCTAGCCAT 1950
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Db 1951 TCCATAGTGTCTCCTTTTGTATGTCGAGATTATGCTGATTTTAAAGAAATGATGAC 2010
Qy 1430 AAAATCTACA 1439
Db 2011 AAAATCTACA 2020

RESULT 12
US-09-981-915A-617
Sequence 617, Application US/09981915A
Publication No. US20030054986A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Deenoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Geritsen, Mary E.
APPLICANT: Goddard, Audrey J.
APPLICANT: Grimaldi, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J
APPLICANT: Kljavin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumes, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630P1C12
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CURRENT FILING DATE: 2001-10-16
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Query Match 37.2%; Score 742; DB 10; Length 2558;
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Matches 1142; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

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871 GACCTGCTGACTACTTCTCTCTGGGGTGAAGTCTTATCCAGACGTTGGAATCTTCT 930

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1051 CCAAGTATTCCTGCTTCATCCAGTTGATCTATGATGTCAGAGAGCTCTAGAAAAATG 1110

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1111 GGTGGCTGACACCAACAGATGACGCTGAGAGAGAGTCTCAAAGTCTTCAATGTT 1170

590 GGAAGTGGCTTTCTGGAATCTTTTCTACACAAAAGTCAAGATGCACATCCACTACC 649
1171 GGAAGTGGCTTTCTGGAATCTTTTCTACACAAAAGTCAAGATGCACATCCACTACC 1230

650 AATGAAGTGAAGAAATTTTCAATGTGATGCTTCTGAGAGAGAGTGAACAGAC 709
1231 AATGAAGTGAAGAAATTTTCAATGTGATGCTTCTGAGAGAGAGTGAACAGAC 1290

710 AGATATGCTATTTGGAGAGTCAACGGGACTATGAGGTTTGGTATTTGACCTCAG 769
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770 AGTGAAGCAGCTTTTCTGATGAACTGTGAGAGCTTTGGAACACTGAAAAAGAGGG 829
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830 TGGAGACTTGAAGAAATTTTGTGCAAGCTGGAATGCAAGAAATTTGCTCTT 889
1411 TGGAGACTTGAAGAAATTTTGTGCAAGCTGGAATGCAAGAAATTTGCTCTT 1470

890 GGTTCACAGAGGGGCAAGGATTAATCAAGCTCTTCAAGAGGCTGGCGTGTAT 949
1471 GGTTCACAGAGGGGCAAGGATTAATCAAGCTCTTCAAGAGGCTGGCGTGTAT 1530

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Db 1531 ATTAATGCTGATCTATCTATGAGAAACCTACCTGAGAGTTGATGACACCGCTG 1590
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Qy 1070 GGCAGAACTCTTTTGAAGTTGGAGCTAAAAAGTCCCTCCAGAGTTGAGTGGCATG 1129
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Qy 1250 CCACTGATACAGTGTCTATGAAACATATGATGTTGGGAAAGTTTATGATCCATG 1309
Db 1831 CCACTGATACAGTGTCTATGAAACATATGATGTTGGGAAAGTTTATGATCCATG 1890
Qy 1310 TTTAAATATCAGCTCACTGTGGCCAGGTTGAGAGGAGATGTTTGAAGTACCAAT 1369
Db 1891 TTTAAATATCAGCTCACTGTGGCCAGGTTGAGAGGAGATGTTTGAAGTACCAAT 1950
Qy 1370 TCCATAGTCTCCCTTTTGTATGTCAGATTAATCTGATTTTAAAGAAATGCTGAC 1429
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Qy 1430 AAAATCTACA 1439
Db 2011 AAAATCTACA 2020

RESULT 13

US-09-978-824-617
Sequence 617, Application US/09978824
Publication No. US20030055216A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Bacon, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerltsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gunney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kijavitt, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630P1C14
CURRENT APPLICATION NUMBER: US/09/978, 824
CURRENT FILING DATE: 2001-10-17

PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
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PRIOR FILING DATE: 1997-11-03
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PRIOR APPLICATION NUMBER: 60/085573
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085704
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085697

Query Match 37.2%; Score 742; DB 10; Length 2558;

Best Local Similarity 99.3%; Pred. No. 0; Mismatches 8; Indels 0; Gaps 0;

Matches 1142; Conservative 0;

QY 290 GACCTGCTGACTACTTCTGCTCTGCGGTGAAGTCTTATCCAGACGCTTGAATCTTCT 349
DB 871 GACCTGCTGACTACTTCTGCTCTGCGGTGAAGTCTTATCCAGACGCTTGAATCTTCT 930
QY 350 GGAAGTGTGTCCAGCGTGAATATCTTAATCTGAATGTGCGAGAACCTCTCA 409
DB 931 GGAAGTGTGTCCAGCGTGAATATCTTAATCTGAATGTGCGAGAACCTCTCA 990
QY 410 CCAGTTACCCAGCAATGAATACGCTTATAGGCATGAATTCAGAGGCTGTGCTT 469
DB 991 CCAGTTACCCAGCAATGAATATGCTTATAGCGTGAATTCAGAGGCTGTGCTT 1050
QY 470 CCAGTTATCTGTTTCATCCAGTTGATATGATGACAGAGCTCTAGAAAAATG 529
DB 1051 CCAGTTATCTGTTTCATCCAGTTGATATGATGATGATGACAGAGCTCTAGAAAAATG 1110
QY 530 GGTGCTCAGCACACCAATGACGCTGGAAGAGAGTCTCAAGTGTCTTCAATGTT 589
DB 1111 GGTGCTCAGCACACCAATGACGCTGGAAGAGAGTCTCAAGTGTCTTCAATGTT 1170
QY 590 GGAAGTGTGTCTGGAAGTCTTCTACACAAAAAGTCAAGTGCATCTTAC 649
DB 1171 GGAAGTGTGTCTGGAAGTCTTCTACACAAAAAGTCAAGTGCATCTTAC 1230
QY 650 AATGAAGTGCAGAAATTTACATGATGATGATCTCAGAGAGCAGTGAACAGAC 709
DB 1231 AATGAAGTGCAGAAATTTACATGATGATGATGATCTCAGAGAGCAGTGAACAGAC 1290
QY 710 AGATATGTCATTTGGAAGTCAACGGGACTATGGGTGTGTTGTTGATTTGACCTCAG 769
DB 1291 AGATATGTCATTTGGAAGTCAACGGGACTATGGGTGTGTTGTTGATTTGACCTCAG 1350
QY 770 AGTGAAGCAGCTGTTGTTGATGAACCTGAGAGCTTTGGAACCTGAAAAAGAGG 829
DB 1351 AGTGAAGCAGCTGTTGTTGATGAACCTGAGAGCTTTGGAACCTGAAAAAGAGG 1410
QY 830 TGAAGACTGAAGAACAAATTTGTTGCAAGCTGGAGTGCAGAAATTTGCTTCTT 889
DB 1411 TGAAGACTGAAGAACAAATTTGTTGCAAGCTGGAGTGCAGAAATTTGCTTCTT 1470
QY 890 GGTTCCTAGAGTGGGCAAGATTAATTAAGACTCTTCAAGAGGCTGGCTGTAT 949
DB 1471 GGTTCCTAGAGTGGGCAAGATTAATTAAGACTCTTCAAGAGGCTGGCTGTAT 1530
QY 950 AATTAAGCTGACCTACTATGAAGAACTACTCTGAGAGTTGATTTGATCAGCAG 1009
DB 1531 AATTAAGCTGACCTACTATGAAGAACTACTCTGAGAGTTGATTTGATCAGCAG 1590
QY 1010 ATGTACAGCTGTGATATACAACTTAACAAAAGAGCTGAAAAAGCCTGATGAGCTTTGAA 1069

Db 1591 ATGACAGCTTGATACAACTAACAAAGAGCGGAAAGCCCGATGAGGCTTGA 1650
Qy 1070 GGCAATCTCTTTATGAAAGTTGACATAAAAAAGTCTTCCCAAGTCAATGGCATG 1129
Db 1651 GGCAATCTCTTTATGAAAGTTGACATAAAAAAGTCTTCCCAAGTCAATGGCATG 1710
Qy 1130 CCCAGATTAAGCAATGGGATCTGAAATATTTTGAAGTGTCTTCCAAAGCATGGA 1169
Db 1711 CCCAGATTAAGCAATGGGATCTGAAATATTTTGAAGTGTCTTCCAAAGCATGGA 1770
Qy 1190 ATTCCTTCAGGACAGACGCGTATATTAATAATTGGAAACAAATTCAGCGCTAT 1249
Db 1771 ATTCCTTCAGGACAGACGCGTATATTAATAATTGGAAACAAATTCAGCGCTAT 1830
Qy 1250 CCACTGATATCACTATGCTATGAAACATATAGTTGGTGGAAAAAGTTTATGATCCATG 1309
Db 1831 CCACTGATATCACTATGCTATGAAACATATAGTTGGTGGAAAAAGTTTATGATCCATG 1890
Qy 1310 TTAAATATCACTCACTGTCGCGCCAGGTTGAGAGAGGATGATTTGAGCTAGCCAT 1369
Db 1891 TTAAATATCACTCACTGTCGCGCCAGGTTGAGAGAGGATGATTTGAGCTAGCCAT 1950
Qy 1370 TCCATAGTGTCTCTTTGATTTGATGATTAATCTGATTTTAAAGAAATAGCTGAC 1429
Db 1951 TCCATAGTGTCTCTTTGATTTGATGATTAATCTGATTTTAAAGAAATAGCTGAC 2010
Qy 1430 AAAATCTACA 1439
Db 2011 AAAATCTACA 2020

RESULT 14

US-09-918-585A-617
Sequence 617, Application US/09918585A
Publication No. US20030060406A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Deenoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gutney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Nadler, Mary A.
APPLICANT: Pan, James,
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630P1C1
CURRENT APPLICATION NUMBER: US/09/918,585A
CURRENT FILING DATE: 2001-07-30
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PRIOR FILING DATE: 1997-10-17
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PRIOR APPLICATION NUMBER: 60/085697
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/086023

Query Match 37.2%; Score 742; DB 10; Length 2558;
Best Local Similarity 99.3%; Pred. No. 0;
Matches 1142; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

290 GACCCCTGACACTTCTGCTGCGGAGTCCATCCAGAGCTTGAATCTTCC 349
871 GACCCCTGACACTTCTGCTGCGGAGTCCATCCAGAGCTTGAATCTTCC 930
350 GGAGTGTGTCCAGGCTGGAATATCTTAATCTGAATGTGACAGAGACCTCTCACA 409
931 GGAGTGTGTCCAGGCTGGAATATCTTAATCTGAATGTGACAGAGACCTCTCACA 990
410 CCAGTTACCCAGCAATGAATACGCTTATAGCATGAATTCAGAGCTGTGTCTT 469
991 CCAGTTACCCAGCAATGAATACGCTTATAGCATGAATTCAGAGCTGTGTCTT 1050
470 CCAAGTATCCGTTGATCCAGTTGATGATGACAGAGGCTCCAGAAAAATG 529
1051 CCAAGTATCCGTTGATCCAGTTGATGATGACAGAGGCTCCAGAAAAATG 1110
530 GGTGCTCAGCACCAAGATGACAGTGAAGTCTCAAGTGTCTTCAATGTT 589
1111 GGTGCTCAGCACCAAGATGACAGTGAAGTCTCAAGTGTCTTCAATGTT 1170
590 GGAAGTGTCTTATGGAATCTTTTACCAAAAAGTCAAGTGCACATCCACTTACC 649
1171 GGAAGTGTCTTATGGAATCTTTTACCAAAAAGTCAAGTGCACATCCACTTACC 1230
650 AATGAAGTGCAGGAATTTTACATGATGACTCTCAGAGGACAGTGAACAGAC 709
1231 AATGAAGTGCAGGAATTTTACATGATGACTCTCAGAGGACAGTGAACAGAC 1290
710 AGATATGTCATTTGGAAGTGCACCGGACTCATGAGTGTGTGTGATTTAGCCCTCAG 769
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770 AGTGAAGCAGCTGTGTGTGTAATCTGGAAGCTTTGGAACATGAAAAAGAAAGG 829
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950 ATTAATGCTGACTCATCTATTAAGAGAACCTACCTCTGAGAGTATTTATACCACTG 1009
1531 ATTAATGCTGACTCATCTATTAAGAGAACCTACCTCTGAGAGTATTTATACCACTG 1590
1010 ATGTACAGCTGTGTATTAACAACCTAACAAGAGCTGAAGAGCTTGAAGAGCTTTGAA 1069
1591 ATGTACAGCTGTGTATTAACAACCTAACAAGAGCTGAAGAGCTTGAAGAGCTTTGAA 1650
1070 GGCAATCTCTTATGAAGTGAATAAAAAAGTCTTCCAGAGTTCAAGTGCAATG 1129

Db 1651 GGCAATCTCTTATGAAAGTTGGACTAAAAAGCTCTCCAGAGTTGAGTGGCATG 1710
Qy 1130 CCCGAGTAAACCAATTGGGATCTGGAATGATTTTGGGTTCTTCCAGACTTGA 1189
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Qy 1190 ATTCCTCAGGAGAGAGAGGATATCTAAAAATTGGGAAACAAATTGAGGGGCTAT 1249
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Qy 1250 CCACGTATCAAGTGTCTATGAAACATATGATGTGTGAAAAATTATGATCCATG 1309
Db 1831 CCACGTATCAAGTGTCTATGAAACATATGATGTGTGAAAAATTATGATCCATG 1890
Qy 1310 TTATAATATCACTCTGTCGCCCCAGTTGAGAGAGGATGTGTTGAGCTAGCCAT 1369
Db 1891 TTATAATATCACTCTGTCGCCCCAGTTGAGAGAGGATGTGTTGAGCTAGCCAT 1950
Qy 1370 TCATAGTCTCCCTTTTGTGATTTGAGATTATGCTGATTTTAAAGAAATGCTGAC 1429
Db 1951 TCATAGTCTCCCTTTTGTGATTTGAGATTATGCTGATTTTAAAGAAATGCTGAC 2010
Qy 1430 AAAATCTACA 1439
Db 2011 AAAATCTACA 2020

RESULT 15

US-09-978-423A-617

Sequence 617, Application US/09978423A

Publication No. US20030069178A1

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerlitsen, Mary E.
APPLICANT: Goddard, Audrey
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APPLICANT: Gurney, Austin L.
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APPLICANT: Kijavini, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tuma, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630P1C1
CURRENT APPLICATION NUMBER: US/09/978,423A
PRIOR FILING DATE: 2002-05-16
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13

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PRIOR FILING DATE: 1998-03-12
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 PRIOR APPLICATION NUMBER: 60/085697

Query Match 37.2%; Score 742; DB 10; Length 2558;
 Best Local Similarity 99.3%; Pred. No. 0;
 Matches 1142; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

290 GACCTGCTGACTACTCTTCTCTCTGGGAGTGAAGTCTTATCCAGACCGTTGAATCTTCT 349
 871 GACCTGCTGACTACTCTTCTCTCTGGGAGTGAAGTCTTATCCAGACCGTTGAATCTTCT 930
 350 GGAGGTGGTCCAGCGTGAATAATCTTAATCTGAATGGTGCAGAGACCCCTCACA 409
 931 GGAGGTGGTCCAGCGTGAATAATCTTAATCTGAATGGTGCAGAGACCCCTCACA 990
 410 CCAGGTTACCCAGCAATGAATAGCTTTATAGGATGAAATTCAGAGCGTGTGCTT 469
 991 CCAGGTTACCCAGCAATGAATAGCTTTATAGGATGAAATTCAGAGCGTGTGCTT 1050
 470 CCAGGTTACCCAGCAATGAATAGCTTTATAGGATGAAATTCAGAGCGTGTGCTT 529
 1051 CCAGGTTACCCAGCAATGAATAGCTTTATAGGATGAAATTCAGAGCGTGTGCTT 1110
 530 GGAGGTGGTCCAGCGTGAATAATCTTAATCTGAATGGTGCAGAGACCCCTCACA 589
 1111 GGAGGTGGTCCAGCGTGAATAATCTTAATCTGAATGGTGCAGAGACCCCTCACA 1170
 590 GGAGGTGGTCCAGCGTGAATAATCTTAATCTGAATGGTGCAGAGACCCCTCACA 649
 1171 GGAGGTGGTCCAGCGTGAATAATCTTAATCTGAATGGTGCAGAGACCCCTCACA 1230
 650 AATGAAGTGAAGCAATTTTACATGATGATGATCTCTCAGAGAGACGTGAAACCAAGC 709
 1231 AATGAAGTGAAGCAATTTTACATGATGATGATCTCTCAGAGAGACGTGAAACCAAGC 1290
 710 AGATATGATCTTGGGAGGTCACCGGACCTCATGAGGTTGGTGTATTTGACCTCTAG 769
 1291 AGATATGATCTTGGGAGGTCACCGGACCTCATGAGGTTGGTGTATTTGACCTCTAG 1350
 770 AGTGAAGCAGCTGTTGTCATGAATCTGTAGAGCTTTGGAACACTGAAAAAGAGGG 829
 1351 AGTGAAGCAGCTGTTGTCATGAATCTGTAGAGCTTTGGAACACTGAAAAAGAGGG 1410
 830 TGAAGCTTGAAGCAATTTTGTTCAGCTGGGATGTCAGAAATTTGGTCTTCTT 889
 1411 TGAAGCTTGAAGCAATTTTGTTCAGCTGGGATGTCAGAAATTTGGTCTTCTT 1470
 890 GGTTCACAGAGGGGAGAGGATTAATCAAGCTCTTCAAGAGGCGGCGCTAT 949
 1471 GGTTCACAGAGGGGAGAGGATTAATCAAGCTCTTCAAGAGGCGGCGCTAT 1530
 950 ATTAATGCTGACTCATCTATAGAGAACTACCTGAGAGTTGATGACCACTG 1009
 1531 ATTAATGCTGACTCATCTATAGAGAACTACCTGAGAGTTGATGACCACTG 1590
 1010 ATTTACAGCTTGTGATACCACTAACAAAGAGCTGAAAGCCCTGATGAGCTTTGAA 1069
 1591 ATTTACAGCTTGTGATACCACTAACAAAGAGCTGAAAGCCCTGATGAGCTTTGAA 1650
 1070 GGCATATCTCTTATGAAGTTGGACTAATAAAGCTTCCCAAGTTCAAGTTCAGTGCATG 1129
 1651 GGCATATCTCTTATGAAGTTGGACTAATAAAGCTTCCCAAGTTCAAGTTCAGTGCATG 1710
 1130 CCAGATTAAGCAATTTGGATCTGAAATGATTTGAGGTGTTCTTCAACAGACTTGA 1189

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         CCCAGATTAAGCAATTGGATCTGAAATGATTTTGGAGTGTCTTCCACGACTTGA 1770  
QY      1190  |||||  
         ATTGCTTCAGGCAGACGCGTATATCTTAAATTTGGAAACAAACAAATTCAGCGCTAT 1249  
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QY      1250  |||||  
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Db      1831  |||||  
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QY      1310  |||||  
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Db      1891  |||||  
         TTAAATATCACTCACTGTGCCCCCAGGTTGAGAGGAGATGTGTTGAGCTAGCCAAT 1950  
QY      1370  |||||  
         TCCATAGTGTCCCTTTTGAATGTCGAGATTATGCTGTAGTTTAAAGAAATATGCTGAC 1429  
Db      1951  |||||  
         TCCATAGTGTCCCTTTTGAATGTCGAGATTATGCTGTAGTTTAAAGAAATATGCTGAC 2010  
QY      1430  |||||  
         AAAATCTACA 1439  
Db      2011  |||||  
         AAAATCTACA 2020
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Search completed: February 17, 2004, 20:00:55
Job time : 1270 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 17, 2004, 16:54:29 ; Search time 3553 Seconds
(without alignments)
16742.320 Million cell updates/sec

Title: US-09-973-382C-1
Perfect score: 1992
Sequence: 1 agcaatactactactaccaca.....taaaaaaaaaaaaaaaaaa 1992

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 27513289 seqs, 14931090276 residues

Word size : 0

Total number of hits satisfying chosen parameters: 55026578
Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

EST:
1: em_estba:*
2: em_estbun:*
3: em_estin:*
4: em_estnu:*
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6: em_estpl:*
7: em_estro:*
8: em_hic:*
9: gb_est1:*
10: gb_est2:*
11: gb_hic:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
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16: em_estom:*
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20: em_gse_vrt:*
21: em_gse_fun:*
22: em_gse_mam:*
23: em_gse_mus:*
24: em_gse_pro:*
25: em_gse_rtd:*
26: em_gse_phg:*
27: em_gse_vtl:*
28: gb_gse1:*
29: gb_gse2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	529	26.6	776	12	BG208080 RST27570
2	460	23.1	1201	9	AL532732 AL532732
3	424	21.3	889	14	CA489536 AGENCOURT
4	414	20.8	885	14	CA976138 AGENCOURT

5	414	20.8	916	14	CA488428	CA488428 AGENCOURT
6	383	19.2	563	10	AW951407	AW951407 EST363477
7	349	17.5	1201	9	AL563970	AL563970 AL563970
8	306	15.4	390	9	AA435800	AA435800 zc78a10.s
9	294	14.8	1201	9	AL532691	AL532691 AL532691
10	284	14.3	305	12	BG203378	BG203378 RST27559
11	281	14.1	797	12	BG202823	BG202823 RST22191
12	279	14.0	508	14	CB216928	CB216928 NISC.nq10
13	276	13.9	757	12	BG194269	BG194269 RST13413
14	242	12.1	427	12	CF135099	CF135099 UI-HF-CB0
15	229	11.5	432	14	CF141546	CF141546 UI-HF-CB0
16	227	11.4	657	14	CF146657	CF146657 UI-HF-CB0
17	223	11.2	625	12	BG206102	BG206102 RST25537
18	221	11.1	474	10	AW945136	AW945136 EST361329
19	201	10.1	653	14	CF146985	CF146985 UI-HF-CB0
20	189	9.5	323	9	AA370337	AA370337 EST82019
21	175	8.8	319	14	CF139418	CF139418 UI-HF-CB0
22	165	8.3	319	14	CF146112	CF146112 UI-HF-CB0
23	158	7.9	296	9	AA371450	AA371450 EST83235
24	156	7.9	681	14	CF145338	CF145338 UI-HF-CB0
25	150	7.5	321	12	BG221564	BG221564 RST41377
26	149	7.5	426	9	AW000926	AW000926 w790e01.x
27	149	7.5	442	14	N48056	N48056 yy99c12.81
28	149	7.5	471	9	AI356718	AI356718 gy17a12.x
29	149	7.5	474	9	AI474492	AI474492 th21d01.x
30	149	7.5	478	10	AM207840	AM207840 UI-H-B12
31	149	7.5	545	12	BQ227857	BQ227857 UI-H-CO0
32	149	7.5	548	10	BF438644	BF438644 nab89b03.
33	149	7.5	618	9	AI766427	AI766427 wh49n09.x
34	149	7.5	690	9	AI672408	AI672408 ey64g12.x
35	149	7.5	770	9	AI050871	AI050871 oy47b11.x
36	145	7.3	452	14	N64840	N64840 yz31h07.81
37	143	7.2	909	13	BQ248549	BQ248549 AGENCOURT
38	139	7.0	720	10	BF940223	BF940223 nac70c04.
39	138	6.9	492	14	N75691	N75691 yv29h07.x1
40	131	6.6	494	9	AI690667	AI690667 kx15c10.x
41	128	6.4	420	9	AA879028	AA879028 nw87e05.s
42	128	6.4	462	9	AA897668	AA897668 o178c06.8
43	122	6.1	882	14	CF146716	CF146716 UI-HF-CB0
44	117	5.9	352	10	BF673465	BF673465 602136247
45	117	5.9	395	9	AA631303	AA631303 ng90g07.s

ALIGNMENTS

RESULT 1
LOCUS BG208080/c
DEFINITION RST27570 Atherys RAGE Library Homo sapiens cDNA, mRNA sequence.
ACCESSION BG208080
VERSION BG208080.1 GI:13729767
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R., Cain,S., Leventhal,C., Thornton,M., Ramachandran,R., Whittington,J., Lerner,L., Costanzo,D., McElligott,K., Boozer,S., Maye,R., Smith,E., Veloso,N., Klika,A., Hesse,J., Cothren,K., Lo,K., Otenbacher,J., Danzig,U., and Ducar,M.
TITLE Creation of genome-wide protein expression libraries using random activation of gene expression
JOURNAL Nat. Biotechnol. 19 (5), 440-445 (2001)
MEDLINE 21227151
PUBMED 11329013
COMMENT Contact: Scott J. Cain
Atherys, Inc.
3201 Carnegie Ave, Cleveland, OH 44115, USA
Tel: 216 431 9900
Fax: 216 361 9596

Email: scaln@atersys.com
High quality sequence stop: 453.

FEATURES

source

1. .776
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/cell_line="HT1080"
/clone_1lb="Athersys RAGE Library"
/note="See 'Creation of Genome-wide Protein Expression Libraries using Random Activation of Gene Expression', Nature Biotechnology, in press. Note that even though the cell type indicated is HT1080, since a random activation method was used, these sequence tags are not necessarily expressed in HT1080 under normal circumstances."

ORIGIN

Query Match 26.6%; Score 529; DB 12; Length 776;
Best Local Similarity 99.8%; Pred. No. 4.2e-90;
Matches 579; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1411 TTTAAGAAAGTATGCTGACAAATCTAACAATTTCTATGAACATCCACAGAAATGAA 1470
580 TTTAAGAAAGTATGCTGACAAATCTAACAATTTCTATGAACATCCACAGAAATGAA 521
1471 GACATACAGTTTATCATCTTTGATCACTTTTCTGCGAGTAAATTTTACAGAAATTCG 1530
520 GACATACAGTTTATCATCTTTGATCACTTTTCTGCGAGTAAATTTTACAGAAATTCG 461
1531 TTCCAAAGTTCAG 1590
460 TTCCAAAGTTCAG 401
1591 GATGAATGATCACTCATGTTTCTGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1650
400 GATGAATGATCACTCATGTTTCTGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 341
1651 CAGACCTTTTATAG 1710
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1711 GTCAATCCAG 1770
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1771 GGCCTGGGAG 1830
220 GGCCTGGGAG 161
1831 AG 1890
160 AG 101
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1951 AAATTAAGTTGAATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTAT 1990
40 AAATTAAGTTGAATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTAT 1

RESULT 2
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LOCUS AL532732 Homo sapiens ADULT BRAIN Homo sapiens cDNA clone
DEFINITION CS0DN001YK13 5-PRIME, mRNA sequence.
ACCESSION AL532732
VERSION AL532732.2 GI:31070564
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE
1 (bases 1 to 1201)
AUTHORS Li, W.B., Gruber, C., Jesse, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT On Feb 13, 2001 this sequence version replaced gi:12796225.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 Evry cedex - France
Email: seqref@genoscope.cns.fr; Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 5903.r For more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0DN001AF07QPL&cluster=5903.r. Contact :
Feng Liang Email: fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0DN001AF07QPL.

FEATURES

source

1. 1201
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/clone="CS0DN001YK13"
/issue_type="ADULT BRAIN"
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/clone_1lb="Homo sapiens ADULT BRAIN"
/note="Organ: Brain; Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was not normalized."

ORIGIN

Query Match 23.1%; Score 460; DB 9; Length 1201;
Best Local Similarity 99.1%; Pred. No. 2e-77;
Matches 860; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

290 GACCTGCTGACTACTCTTCTCTGGGGTGAAGTCTTATCCAGACGGTTGGATCTTCT 349
125 GACCTGCTGACTACTCTTCTCTGGGGTGAAGTCTTATCCAGACGGTTGGATCTTCT 184
350 GAGAGTGTGTCCAGAGTGAATATCTAATCTGAATGTGACAGAGACCTCTCACA 409
185 GAGAGTGTGTCCAGAGTGAATATCTAATCTGAATGTGACAGAGACCTCTCACA 244
410 CCAGGTTACCCAGCAATGAATACGTTATAGCATGAATTGACAGAGCTGTGTCTT 469
245 CCAGGTTACCCAGCAATGAATATGCTTATAGCGTGAATTGACAGAGCTGTGTCTT 304
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530 GGTGGCTGACACACACAGATAGCAGTGAAGAGAGCTCAAAAGTGTCTCAATGTT 589
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590 GGAAGTGGCTTTTACTGAAATCTTTTCTACACAAAAGTCAAGATGACATCCACTTACC 649
425 GGAAGTGGCTTTTACTGAAATCTTTTCTACACAAAAGTCAAGATGACATCCACTTACC 484
650 AATGAAGTACAGAGATTTTCAATGTGATGATCTCTCAAGAGACATGGAACAGAGC 709
485 AATGAAGTACAGAGATTTTCAATGTGATGATCTCTCAAGAGACATGGAACAGAGC 544
710 AGATATGTCATCTTGGAGAGTACCGGAGCTCATGGGTGTTGGTGTGATTCAGCCTCAG 769
545 AGATATGTCATCTTGGAGAGTACCGGAGCTCATGGGTGTTGGTGTGATTCAGCCTCAG 604
770 AGTGAAGACAGCTGTGTTTCATGAATGTTGAGAGAGCTTTGGAACACTGAAAAGAGAG 829
605 AGTGAAGACAGCTGTGTTTCATGAATGTTGAGAGAGCTTTGGAACACTGAAAAGAGAG 664

Query Match 21.3%; Score 424; DB 14; Length 889;
 Best Local Similarity 99.6%; Pred. No. 1,4e-70;
 Matches 524; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 830 TGGAGACCTAGAGAACAAATTTGTTGCAAGCTGGATGCGAAGAAATTTGCTTCTT 889
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 QY 890 GGTTCCTAGTGGGAGAGAGATTAATCAAGACTCTCTTCAAGAGCGTGGCGTTAT 949
 DB 725 GGTTCCTAGTGGGAGAGAGATTAATCAAGACTCTCTTCAAGAGCGTGGCGTTAT 784
 QY 950 ATTAATGCTGATCTATATAGAGAACTACCTGCTGAGTGTGATGACCCACTG 1009
 DB 785 ATTAATGCTGATCTATATAGAGAACTACCTGAGATGTGATGACCCACTG 844
 QY 1010 ATGACAGCTGTGATACAACTTAACAAAGAGCTGAAAAGCCCTGATGAAAGCTTGA 1069
 DB 845 ATGACAGCTGTGATACAACTTAACAAAGAGCTGAAAAGCCCTGATGAAAGCTTGA 904
 QY 1070 GGCATAATCTCTTATGAAAGTTGAGCTAAAGAAAGCTCTTCCGAGAGTTCAAGTGCATG 1129
 DB 905 GGCATAATCTCTTATGAAAGTTGAGCTAAAGAAAGCTCTTCCGAGAGTTCAAGTGCATG 964
 QY 1130 CCCAGATTAAGCAATTTGGATCTGGAA 1157
 DB 965 CCCAGATTAAGCAATTTGGATCTGGAA 992

RESULT 3
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LOCUS AGENCOURT_10810626 MAFCL Homo sapiens cDNA clone IMAGE:6722010 5',
 ACCESSION CA489536
 VERSION CA489536
 KEYWORDS EST.

SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 889)

NIH-MGC http://mgc.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 CONTACT: Robert Strausberg, Ph.D.
 Email: cgabs-remail.nih.gov
 Tissue Procurement: Kristi A. Egland, Ira Pastan
 CDNA Library Preparation: Invitrogen Corp
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov

Plate: LHAM14284 row: a column: 18
 High quality sequence stop: 670.
 Location/Qualifiers

FEATURES
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 HTERT-HME1, LNCaP"
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 /note="Vector: pCMV-SPORT6, Site 1: EcoRV, Site 2: Not I;
 Subcloned with brain, liver, lung, kidney and muscle.
 Directionally cloned. Priming method: oligo-dT. Average
 insert size: 1800 bp. Library amplification: 26,000 fold.
 Kristi A. Egland, James J. Vincent, Robert Strausberg,
 Bunkook Lee & Ira Pastan. Discovery of new breast
 cancer genes encoding membrane and secreted proteins.
 Manuscript submitted."

ORIGIN

Query Match 21.3%; Score 424; DB 14; Length 889;
 Best Local Similarity 99.6%; Pred. No. 1,4e-70;
 Matches 524; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 914 AATTCAGACTCTCTTCAAGAGCGTGGCGTTATATTAATGCTGATCTATAGAA 973
 DB 39 AATTCAGACTCTCTTCAAGAGCGTGGCGTTATATTAATGCTGATCTATAGAA 98
 QY 974 GGAACCTACCTGAGAGTTGATTTGATACCCACTGATGATGACGCTTGTATCAACTTA 1033
 DB 99 GGAACCTACCTGAGAGTTGATTTGATACCCACTGATGATGACGCTTGTATCAACTTA 158
 QY 1034 ACAAAAGAGCTGAAAAGCCCTGATGAAAGCTTGAAGCAATCTCTTATGAAAGTTGG 1093
 DB 159 ACAAAAGAGCTGAAAAGCCCTGATGAAAGCTTGAAGCAATCTCTTATGAAAGTTGG 218
 QY 1094 ACTAAAAAGCTCTTCCCGAGATTCAAGTGCATGCCAGATTAAGCAATTTGGATCT 1153
 DB 219 ACTAAAAAGCTCTTCCCGAGATTCAAGTGCATGCCAGATTAAGCAATTTGGATCT 278
 QY 1154 GGAATGATTTTGAAGTGTCTTCCACGACTTGAATGCTTCAAGCAGACGCTAT 1213
 DB 279 GGAATGATTTTGAAGTGTCTTCCACGACTTGAATGCTTCAAGCAGACGCTAT 338
 QY 1214 ACTAAAAATTTGGAAAACAACAATTCAGCGGCTATCCACTGATCAAGTGTCTATGAA 1273
 DB 339 ACTAAAAATTTGGAAAACAACAATTCAGCGGCTATCCACTGATCAAGTGTCTATGAA 398
 QY 1274 ACATATGAGTTGTGGAAGAGTTTATGATCAATGTTTAAATATCACTCACTGTGGCC 1333
 DB 399 ACATATGAGTTGTGGAAGAGTTTATGATCAATGTTTAAATATCACTCACTGTGGCC 458
 QY 1334 CAGGTCGAGAGAGAGATGTTGTTGAGCTTGAAGCCAAATTCATGCTCTCTTTGATGT 1393
 DB 459 CAGGTCGAGAGAGAGATGTTGTTGAGCTTGAAGCCAAATTCATGCTCTCTTTGATGT 518
 QY 1394 CGAGATTATGCTGTAGTTTAAAGAAATGCTGACAAATCTACA 1439
 DB 519 CGAGATTATGCTGTAGTTTAAAGAAATGCTGACAAATCTACA 564

RESULT 4
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 LOCUS AGENCOURT_8955013 Lupsk1_sciatic_nerve Homo sapiens cDNA clone
 IMAGE:6202554 5', mRNA sequence.
 ACCESSION CA976138
 VERSION CA976138.1 GI:27508792
 KEYWORDS EST.

SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 885)
 NIH-MGC http://mgc.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 CONTACT: Robert Strausberg, Ph.D.
 Email: cgabs-remail.nih.gov
 Tissue Procurement: Dr. James R. Lupski
 CDNA Library Preparation: Life Technologies, Inc.
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LHAM13620 row: m column: 19
 High quality sequence stop: 643.
 Location/Qualifiers

FEATURES
 source

1. 885
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/clone="IMAGE:6202554"
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 /dev_stage="adult, 70 Yr"
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 /clone_lib="Lupski, sciatic nerve"
 /notes="Vector: PCMV-SPORT6 (Life Technologies); Site_1:
 NotI; Site_2: SalI; cDNA made by oligo-dT priming;
 directionally cloned using the following adaptors:
 5'-TCGACCCAGCGCTCCG-3' and
 5'-GACTAGTTCAGATCGGAGCGGCCCT(15)-3'. Size selected >
 1 kb for average insert length 1.87 kb. This is a primary
 library, non-amplified. Library constructed by Life
 Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor
 College of Medicine) and is available through Life
 Technologies."

ORIGIN

Query Match 20.8%; Score 414; DB 14; Length 885;
 Best Local Similarity 100.0%; Pred. No. 1e-68;
 Matches 414; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1026 ACAACCTAACAAAGAGCTGAAAAAGCCCTGATGAGGCTTTGAAAGCAATCTTTATG 1085
 DB 51 ACAACCTAACAAAGAGCTGAAAAAGCCCTGATGAGGCTTTGAAAGCAATCTTTATG 110
 QY 1086 AAGTTGAGTAAAAAAGTCTTCCCAAGTTCATGCGCATGCCAGATAAGCAAT 1145
 DB 111 AAGTTGAGTAAAAAAGTCTTCCCAAGTTCATGCGCATGCCAGATAAGCAAT 170
 QY 1146 TGGGATCGAAAAATGATTTGAGGTGTTCTTCCACAGCTGGAATGCTTCAGCAGAG 1205
 DB 171 TGGGATCGAAAAATGATTTGAGGTGTTCTTCCACAGCTGGAATGCTTCAGCAGAG 230
 QY 1206 CAGGTAATCTAAAAATTGGGAAACAAACAAATTCACGGCTATCCATGATCAGTG 1265
 DB 231 CAGGTAATCTAAAAATTGGGAAACAAACAAATTCACGGCTATCCATGATCAGTG 290
 QY 1266 TCTATGAAACATATGATGTTGGTGAAGTTTATGATCCAAATGTTAAATACACTCA 1325
 DB 291 TCTATGAAACATATGATGTTGGTGAAGTTTATGATCCAAATGTTAAATACACTCA 350
 QY 1326 CTGTGGCCAGGTTCCAGAGAGGATGTTGTTGAGTACGCAATTCATAGTCTCCCT 1385
 DB 351 CTGTGGCCAGGTTCCAGAGAGGATGTTGTTGAGTACGCAATTCATAGTCTCCCT 410
 QY 1386 TTGATTGTGAGATTATGCTGTAGTTTAAAGAAAGTATGCTGACAAATCTACA 1439
 DB 411 TTGATTGTGAGATTATGCTGTAGTTTAAAGAAAGTATGCTGACAAATCTACA 464

RESULT 5
 LOCUS CA488428 916 bp mRNA linear EST 14-NOV-2002
 DEFINITION AGENCOURT 10809202 MAFCL Homo sapiens cDNA clone IMAGE:6720185 5',
 mRNA sequence.
 ACCESSION CA488428
 VERSION CA488428.1 GI:24950277
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 916)
 NIH-MGC http://mgc.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Kristi A. Eglund, Ira Pastan
 cDNA Library Preparation: Invitrogen Corp
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINTL)
 DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LINTL at:
<http://image.jnl.gov>
 Plate: LHAM14279 row e column: 17
 High quality sequence stop: 448.
 Location/Qualifiers

FEATURES

source

1. 916
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:6720185"
 /cell_line="ZR-75-1, MCF7, SK-BR-3, MDA-MB-231,
 HTER1-HM1, LNCaP"
 /lab_host="EMDH10B"
 /clone_lib="MAPEL"
 /notes="Vector: PCMV-SPORT6; Site_1: EcoRV; Site_2: Not I;
 Subtracted with brain, liver, lung, kidney and muscle.
 Directionally cloned. Priming method: oligo-dT. Average
 insert size: 1800 bp. Library amplification: 26,000 fold.
 Kristi A. Eglund, James J. Vincent, Robert Strausberg,
 Bungkok Lee & Ira Pastan: Discovery of new breast
 cancer genes encoding membrane and secreted proteins.
 Manuscript submitted."

ORIGIN

Query Match 20.8%; Score 414; DB 14; Length 916;
 Best Local Similarity 100.0%; Pred. No. 9.8e-69;
 Matches 414; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1026 ACAACCTAACAAAGAGCTGAAAAAGCCCTGATGAGGCTTTGAAAGCAATCTTTATG 1085
 DB 42 ACAACCTAACAAAGAGCTGAAAAAGCCCTGATGAGGCTTTGAAAGCAATCTTTATG 101
 QY 1086 AAGTTGAGTAAAAAAGTCTTCCCAAGTTCATGCGCATGCCAGATAAGCAAT 1145
 DB 102 AAGTTGAGTAAAAAAGTCTTCCCAAGTTCATGCGCATGCCAGATAAGCAAT 161
 QY 1146 TGGGATCGAAAAATGATTTGAGGTGTTCTTCCACAGCTGGAATGCTTCAGCAGAG 1205
 DB 162 TGGGATCGAAAAATGATTTGAGGTGTTCTTCCACAGCTGGAATGCTTCAGCAGAG 221
 QY 1206 CAGGTAATCTAAAAATTGGGAAACAAACAAATTCACGGCTATCCATGATCAGTG 1265
 DB 222 CAGGTAATCTAAAAATTGGGAAACAAACAAATTCACGGCTATCCATGATCAGTG 281
 QY 1266 TCTATGAAACATATGATGTTGGTGAAGTTTATGATCCAAATGTTAAATACACTCA 1325
 DB 282 TCTATGAAACATATGATGTTGGTGAAGTTTATGATCCAAATGTTAAATACACTCA 341
 QY 1326 CTGTGGCCAGGTTCCAGAGAGGATGTTGTTGAGTACGCAATTCATAGTCTCCCT 1385
 DB 342 CTGTGGCCAGGTTCCAGAGAGGATGTTGTTGAGTACGCAATTCATAGTCTCCCT 401
 QY 1386 TTGATTGTGAGATTATGCTGTAGTTTAAAGAAAGTATGCTGACAAATCTACA 1439
 DB 402 TTGATTGTGAGATTATGCTGTAGTTTAAAGAAAGTATGCTGACAAATCTACA 455

RESULT 6
 LOCUS AW951407 563 bp mRNA linear EST 01-JUN-2000
 DEFINITION EST363477 MAGE resequences, MAGB Homo sapiens cDNA, mRNA sequence.
 ACCESSION AW951407
 VERSION AW951407.1 GI:8141080
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 563)
 Hegde, P., Qi, R., Abernathy, K., Dharap, S., Gaspard, R., Gay, C.,
 Holt, I. E., Saeed, A. I., Sharov, V., Lee, N. H., Yeatman, T. J. and
 Quackenbush, J.

TITLE Assessment of gene expression patterns in a model of colon tumor metastasis using a 19,200 element cDNA microarray
JOURNAL Unpublished (2000)
COMMENT Contact: John Quackenbush
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 3528
Fax: 301 838 0208
Email: johnq@tigr.org
Plate: 27

Seq primer: Reverse.
Location/Qualifiers
1. .563
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_lib="MAGE resequences, MAGE"
/note="Vector: pBluescriptSKm"

FEATURES
source

ORIGIN

Query Match 19.2%; Score 383; DB 10; Length 563;
Best Local Similarity 100.0%; Pred. No. 9.3e-63;
Matches 383; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1026 ACAACTAACAAGAGCTGAAAGCCCTGATGAAGCTTGAAGCAATCTTTATG 1085
DB 71 ACAACCTAACAAAGAGCTGAAAGCCCTGATGAAGCTTGAAGCAATCTTTATG 130
QY 1086 AAGTTGACTAAAAAAGTCTTCCCGAGATTCAGTGCATGCCAGATTAACAAAT 1145
DB 131 AAGTTGACTAAAAAAGTCTTCCCGAGATTCAGTGCATGCCAGATTAACAAAT 190
QY 1146 TGGGATCGGAAATGATTTGAGGTGTTCTTCAACGACTTGAATGCTTCAGGCAAG 1205
DB 191 TGGGATCGGAAATGATTTGAGGTGTTCTTCAACGACTTGAATGCTTCAGGCAAG 250
QY 1206 CACGCTATCTAAATTTGGGAAACAACAAATTCAGCGCTATCTCATGATCAGTG 1265
DB 251 CACGCTATCTAAATTTGGGAAACAACAAATTCAGCGCTATCTCATGATCAGTG 310
QY 1266 TCTATGAAACATATGAGTTGGTGAAGATTTATGATCCAGTGTAAATATCAGCTCA 1325
DB 311 TCTATGAAACATATGAGTTGGTGAAGATTTATGATCCAGTGTAAATATCAGCTCA 370
QY 1326 CTGTGGCCCGAGTTCGAGGAGGATGCTTTGAGCTAAGCAATTCATATGCTCCCTT 1385
DB 371 CTGTGGCCCGAGTTCGAGGAGGATGCTTTGAGCTAAGCAATTCATATGCTCCCTT 430
QY 1386 TTGATTTGCGAGATTATGCTGTA 1408
DB 431 TTGATTTGCGAGATTATGCTGTA 453

RESULT 7
AL563970/c 1201 bp mRNA linear EST 31-MAY-2003

LOCUS AL563970 Homo sapiens FETAL LIVER Homo sapiens cDNA clone
DEFINITION CS0DM001YE22 3-PRIME, mRNA sequence.

ACCESSION AL563970
VERSION AL563970.2 GI:31287955
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 1201)
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS Li, W.B., Gruber, C., Jesse, J., and Polayes, D.

TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT On Feb 15, 2001 this sequence version replaced gi:12913887.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France

Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 5903.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0DM001BCL1NP1&cluster=5903.r. Contact:
Feng Liang Email: fliang@lifetech.com URL:
http://fulllength.invitrogen.com/Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID: CS0DM001BCL1NP1.

FEATURES
source

Query Match 17.5%; Score 349; DB 9; Length 1201;
Best Local Similarity 100.0%; Pred. No. 9.8e-57;
Matches 349; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

ORIGIN

QY 1091 TGGACTAAAAAAGTCTTCCCGAGATTCAGTGCATGCCAGATTAACAAATTTGGGA 1150
DB 861 TGGACTAAAAAAGTCTTCCCGAGATTCAGTGCATGCCAGATTAACAAATTTGGGA 802
QY 1151 TCTGAAATGATTTGAGGTGTTCTTCAACGACTTGAATGCTTCAGGCAAGCAG 1210
DB 801 TCTGAAATGATTTGAGGTGTTCTTCAACGACTTGAATGCTTCAGGCAAGCAG 742
QY 1211 TATATCTAAATTTGGGAAACAACAAATTCAGCGCTATCTCATGATCAGTGTAT 1270
DB 741 TATATCTAAATTTGGGAAACAACAAATTCAGCGCTATCTCATGATCAGTGTAT 682
QY 1271 GAAACATATGATGTTGGTGAAGATTTATGATCCAAATGTTAAATATCAGCTCAGTG 1330
DB 681 GAAACATATGATGTTGGTGAAGATTTATGATCCAAATGTTAAATATCAGCTCAGTG 622
QY 1331 GCCCAGGTTGAGAGGAGATGTTGTTGAGCTAAGCAATTCATATGCTCCCTTTGAT 1390
DB 621 GCCCAGGTTGAGAGGAGATGTTGTTGAGCTAAGCAATTCATATGCTCCCTTTGAT 562
QY 1391 TGTGAGATTATGCTGATTTTAAAGAAATATGCTGACAAATCTTACA 1439
DB 561 TGTGAGATTATGCTGATTTTAAAGAAATATGCTGACAAATCTTACA 513

RESULT 8
AA435800/c 390 bp mRNA linear EST 09-NOV-1997

LOCUS AA435800
DEFINITION z178a10.s1 Soares, testis NHT Homo sapiens cDNA clone IMAGE:728442
3, similar to gb:U99487 PROSTATE-SPECIFIC MEMBRANE ANTIGEN
(HUMAN); contains Alu repetitive element; mRNA sequence.

ACCESSION AA435800
VERSION AA435800.1 GI:2140714
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 390)
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S.,
Kilman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Maira, M.,
Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F.,
Theising, B., White, Y., Wylie, T., Waterston, R., and Wilson, R.

TITLE Mashu-NCI human EST Project

JOURNAL
COMMENT

Unpublished (1997)
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.wustl.edu
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
Insert Length: 1837 Std Error: 0.00
Seq primer: -41m13 fwd. ET from Amersham
High quality sequence stop: 359.
Location/Qualifiers

FEATURES

source

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1. 390
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:5925355"
/db_xref="taxon:9606"
/clone="IMAGE:728442"
/sex="male"
/lab_host="DH10B"
/clone_lib="Soares testis_NHT"
/notes="Vector: pRT3D-Pac (Pharmacia) with a modified
polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA
was prepared from mRNA obtained from Clontech
Laboratories, Inc., and primed with a Not I - oligo(dT)
primer [5].
TGTACCAATCTGAAGTGGAGGCGGCCCAATTTTCTTTTCTTTT 3'}.
Double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pRT3D vector. Library
went through one round of normalization to Cos's, and was
constructed by Bento Soares and M. Fatima Bonaldo."
```

ORIGIN

Query Match 15.4%; Score 306; DB 9; Length 390;
Best Local Similarity 100.0%; Pred. No. 3e-48;
Matches 306; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1664 AGGCATGTCATCTATGCTCCAGACGACCAACAAAGTATGAGGGAGTCTTCCAGGA 1723
DB 306 AGGCATGTCATCTATGCTCCAGACGACCAACAAAGTATGAGGGAGTCTTCCAGGA 247
QY 1724 ATTTATGATCTCTGTTGATATTTGAAGCAAGTGAACCTTCCAAAGGCTGGGAGAT 1783
DB 246 ATTTATGATCTCTGTTGATATTTGAAGCAAGTGAACCTTCCAAAGGCTGGGAGAT 187
QY 1784 GTGAAGACAGATTTCTGTGACGCTTCACAGTGCAGGACGCTGCAGAGACTTTGAGT 1843
DB 186 GTGAAGACAGATTTCTGTGACGCTTCACAGTGCAGGACGCTGCAGAGACTTTGAGT 127
QY 1844 GAAGTACCTTAAGAGATTTCTTAAGACCTCTGATTAAGTATTTGTGTGATGTCATCA 1903
DB 126 GAAGTACCTTAAGAGATTTCTTAAGACCTCTGATTAAGTATTTGTGTGATGTCATCA 67
QY 1904 AAGAATATATATGGGTATTTGATTAATTTTAAATTTGATATTTTGAATTAAGTGAA 1963
DB 66 AAGAATATATATGGGTATTTGATTAATTTTAAATTTGATATTTTGAATTAAGTGAA 7
QY 1964 TATTAT 1969
DB 6 TATTAT 1
```

RESULT 9
AL532691/c 1201 bp mRNA linear EST 23-MAY-2003
LOCUS AL532691 Homo sapiens ADULT BRAIN Homo sapiens cDNA clone
DEFINITION CS0DN001YK13 3-PRIME, mRNA sequence.
ACCESSION AL532691
VERSION AL532691
KEYWORDS EST.
SOURCE Homo sapiens (human)

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (baes 1 to 1201)
Li, W.B., Gruber, C., Jesse, J., and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On Feb 13, 2001 this sequence version replaced gi:12796184.
COMMENT
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 Evry cedex - France
Email: seq@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 5903.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0DN001AF07NP1&cluster=5903.r. Contact :
Feng Liang Email : fliang@lifestech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Paradise Avenue Genoscope sequence ID : CS0DN001AF07NP1.

FEATURES

source

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1. 1201
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DN001YK13"
/issue_type="ADULT BRAIN"
/dev_stage="adult"
/clone_lib="Homo sapiens ADULT BRAIN"
/notes="Organ: Brain; Vector: pCMVSPORT 6; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-strand cDNA was digested with Not I and
cloned into the Not I and EcoRV sites of the pCMVSPORT 6
vector. Library was not normalized."
```

ORIGIN

Query Match 14.8%; Score 294; DB 9; Length 1201;
Best Local Similarity 99.8%; Pred. No. 1.7e-46;
Matches 414; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

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QY 1026 ACACTTAACAAAGAGCTGAAAGCCCTGATGAGAGGCTTTGAAGCAATCTTTTANG 1085
DB 846 ACACTTAACAAAGAGCTGAAAGCCCTGATGAGAGGCTTTGAAGCAATCTTTTANG 787
QY 1086 AAGTTGGACTAAAGAGCTTCCAGAGTTCAGTGGACATGCCAGATTAAGCAAT 1145
DB 786 AAGTTGGACTAAAGAGCTTCCAGAGTTCAGTGGACATGCCAGATTAAGCAAT 727
QY 1146 TGGGATCTGGAATGATTTTGAAGTGTCTTCCAGACTTGAATTTGCTTCAG-GCAG 1204
DB 726 TGGGATCTGGAATGATTTTGAAGTGTCTTCCAGACTTGAATTTGCTTCAGGCGCAG 667
QY 1205 GCACGGTATCTAAATTTGGGAACAACAAATTCAGCGGCTATCACTGATCAAGT 1264
DB 666 GCACGGTATCTAAATTTGGGAACAACAAATTCAGCGGCTATCACTGATCAAGT 607
QY 1265 GTCATGAACAATATGATTTGGGAAGTTTATGATCAATGTTTAAATATCACTC 1324
DB 606 GTCATGAACAATATGATTTGGGAAGTTTATGATCAATGTTTAAATATCACTC 547
QY 1325 ACTGTGGCCAGGTTGAGAGGAGTGTGTTGAGACTAGCCAAATTCATAGTCTCCT 1384
DB 546 ACTGTGGCCAGGTTGAGAGGAGTGTGTTGAGACTAGCCAAATTCATAGTCTCCT 487
QY 1385 TTGATTTGCGAGATTATGCTGATTTTAAAGAAATATGCTGACAAATCTTCA 1439
DB 486 TTGATTTGCGAGATTATGCTGATTTTAAAGAAATATGCTGACAAATCTTCA 432
```

RESULT 10
BG203378/c 305 bp mRNA linear EST 21-APR-2001
LOCUS BG203378/c
DEFINITION RST22759 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.

ACCESSION BG203378
 VERSION BG203378.1 GI:13725065
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 305)
 AUTHORS Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R., Cain,S., Leventhal,C., Thornton,M., Ramchandran,R., Whittington,J., Letner,L., Costanzo,D., McElligott,K., Booser,S., Mays,R., Smith,E., Veloso,N., Kika,A., Hess,J., Cochren,K., Lo,K., Offenbacher,J., Danzig,J. and Ducar,M.
 TITLE Creation of genome-wide protein expression libraries using random activation of gene expression
 JOURNAL Nat. Biotechnol. 19 (5), 440-445 (2001)
 MEDLINE 21227151
 PUBMED 11329013
 COMMENT Contact: Scott J. Cain
 Athersys, Inc.
 3201 Carnegie Ave, Cleveland, OH 44115, USA
 Tel: 216 431 9900
 Fax: 216 361 9596
 Email: scalc@athersys.com
 High quality sequence stop: 305.
 Location/Qualifiers
 1..305
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /cell_line="HT1080"
 /clone_lib="Athersys RAGE Library"
 /note="See 'Creation of Genome-wide Protein Expression Libraries using Random Activation of Gene Expression', Nature Biotechnology, in press. Note that even though the cell type indicated is HT1080, since a random activation method was used, these sequence tags are not necessarily expressed in HT1080 under normal circumstances."
 ORIGIN
 Query Match 14.3%; Score 284; DB 12; Length 305;
 Best Local Similarity 100.0%; Pred. No. 4.7e-44;
 Matches 284; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1676 TATGCTCAAGCAGCCCAACAAGTATGCGAGGAGTATCCAGAAATTTATGATGCT 1735
 Db 296 TATGCTCAAGCAGCCCAACAAGTATGCGAGGAGTATCCAGAAATTTATGATGCT 237
 QY 1736 CTGTTGATATTTGAAGCAAGTGAACCTTCCAAAGGCTGGGGAGATGGAAGAGACAG 1795
 Db 236 CTGTTGATATTTGAAGCAAGTGAACCTTCCAAAGGCTGGGGAGATGGAAGAGACAG 177
 QY 1796 ATTTCTGTGACGCTTCAAGTGCAGGAGCTGCAGAGACTTGAAGTGAAGCTTAA 1855
 Db 176 ATTTCTGTGACGCTTCAAGTGCAGGAGCTGCAGAGACTTGAAGTGAAGCTTAA 117
 QY 1856 GAGATCTTTAAGAGACTCTGTATGTAATTTGTGTGTATGCTCAAGAAATATATAT 1915
 Db 116 GAGATCTTTAAGAGACTCTGTATGTAATTTGTGTGTATGCTCAAGAAATATATAT 57
 QY 1916 GGGTATATGATTAATTTAAATTTGGTATATTTGAATAAAGT 1959
 Db 56 GGGTATATGATTAATTTAAATTTGGTATATTTGAATAAAGT 13
 RESULT 11
 BG202823 797 bp mRNA linear EST 21-Apr-2001
 LOCUS BRT22191 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.
 DEFINITION BG202823
 ACCESSION BG202823.1 GI:13724510
 VERSION BG202823.1
 KEYWORDS EST.
 SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 797)
 AUTHORS Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R., Cain,S., Leventhal,C., Thornton,M., Ramchandran,R., Whittington,J., Letner,L., Costanzo,D., McElligott,K., Booser,S., Mays,R., Smith,E., Veloso,N., Kika,A., Hess,J., Cochren,K., Lo,K., Offenbacher,J., Danzig,J. and Ducar,M.
 TITLE Creation of genome-wide protein expression libraries using random activation of gene expression
 JOURNAL Nat. Biotechnol. 19 (5), 440-445 (2001)
 MEDLINE 21227151
 PUBMED 11329013
 COMMENT Contact: Scott J. Cain
 Athersys, Inc.
 3201 Carnegie Ave, Cleveland, OH 44115, USA
 Tel: 216 431 9900
 Fax: 216 361 9596
 Email: scalc@athersys.com
 High quality sequence stop: 548.
 Location/Qualifiers
 1..797
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /cell_line="HT1080"
 /clone_lib="Athersys RAGE Library"
 /note="See 'Creation of Genome-wide Protein Expression Libraries using Random Activation of Gene Expression', Nature Biotechnology, in press. Note that even though the cell type indicated is HT1080, since a random activation method was used, these sequence tags are not necessarily expressed in HT1080 under normal circumstances."
 ORIGIN
 Query Match 14.1%; Score 281; DB 12; Length 797;
 Best Local Similarity 99.4%; Pred. No. 6.8e-44;
 Matches 501; Conservative 0; Mismatches 2; Indels 1; Gaps 1;
 QY 1015 CAGCTTGATATCACTTAACAAGAGCTGAAAAGCCCTGATGAAGCTTTGAAGCAA 1074
 Db 114 CAGCTTGATATCACTTAACAAGAGCTGAAAAGCCCTGATGAAGCTTTGAAGCAA 173
 QY 1075 ATCTCTTATGAAGAAGTTGACATTAAGAAAGTCTTCCAGAGTTCAGTGCATGCCAG 1134
 Db 174 ATCTCTTATGAAGAAGTTGACATTAAGAAAGTCTTCCAGAGTTCAGTGCATGCCAG 233
 QY 1135 G-ATAAGCAAAATGGAGATCTGAAAATGATTTTGAAGTCTTCCAAAGCACTTGAATTG 1193
 Db 234 GATTAAGCAAAATGGAGATCTGAAAATGATTTTGAAGTCTTCCAAAGCACTTGAATTG 293
 QY 1194 CTTCAAGGAGACAGGTATCTAATAAATTTGGAAACAACAATTCAGGGCTATCCAC 1253
 Db 294 CTTCAAGGAGACAGGTATCTAATAAATTTGGAAACAACAATTCAGGGCTATCCAC 353
 QY 1254 TGTATCAAGAGTGTATGAACAATATGATGAGTGTGAAAAAGTTTATGATCCAAATTTTA 1313
 Db 354 TGTATCAAGAGTGTATGAACAATATGATGAGTGTGAAAAAGTTTATGATCCAAATTTTA 413
 QY 1314 AATATCACTCACTGAGGCCAGGTTCCAGAGGAGATGAGTGTGAGTGAAGCAATTTCA 1373
 Db 414 AATATCACTCACTGAGGCCAGGTTCCAGAGGAGATGAGTGTGAGTGAAGCAATTTCA 473
 QY 1374 TAGTGCTCCCTTTGATGTCGAGATTATGCTGTATTTAAGAAAGTATGTCACAAA 1433
 Db 474 TAGTGCTCCCTTTGATGTCGAGATTATGCTGTATTTAAGAAAGTATGTCACAAA 533
 QY 1434 TCTACAAATTTTCTATGAACAATCCACAGAAATGAAGACATACAGTTTATTCATTTGATT 1493
 Db 534 TCTACAAATTTTCTATGAACAATCCACAGAAATGAAGACATACAGTTTATTCATTTGATT 593
 QY 1494 CACTTTTCTGCAATAAAAAATT 1517

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Db          594 CACITTTTCTGCAGTAAAAAATT 617
|||||
RESULT 12
LOCUS      CB216928
DEFINITION NISC ng10e02.Y1 NICHd_HS_Ut2 Homo sapiens CDNA clone IMAGE:5938635
ACCESSION CB216928
VERSION    CB216928
KEYWORDS   CB216928.1 GI:28265120
SOURCE     EST.
ORGANISM   Homo sapiens (human)
            Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 508)
            NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
AUTHORS    National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
            Unpublished (1997)
JOURNAL    Contact: Robert Strausberg, Ph.D.
COMMENT    Email: cgapbs-remail.nih.gov
            CDNA Library Preparation:
            DNA Library Arrayed by: The I.M.A.G.E. Consortium/LINL
            Sequencing Center (NISC)
            Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LINL at:
            info@image.lnl.gov
            Plate: LLM1167 row: 1 column: 4
            Seq primer: M13RPL reverse primer (ABI).
            Location/Qualifiers
FEATURES

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FEATURES
source
location/Qualifiers
1..508
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5938635"
/sex="female"
/tissue_type="normal endometrium, mid-secretory phase,
cycle day 23"
/lab_host="DH10B (T1-resistant)"
/clone_lib="NICHD HS Ut2"
/note="Organ: uterus; Vector: pCMV-Sport6.1.cdb (ResGen,
Invitrogen Corporation); Site.1: NotI; Site.2: EcoRV;
Cloned unidirectionally from microquantity amounts of mRNA
from normal endometrial tissue (mid-secretory phase), cycle
day 23). Average insert size 1.6 kb. Library constructed
by ResGen (Invitrogen Corporation)."
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	Query Match	14.0%	Score 279;	DB 14;	Length 508;
	Similarity	99.2%;	Pred. No. 2.5e-43;		
	Matches	479;	Conservative	0;	Mismatches 43;
					Indels 0;
					Gaps 0;
Qy	662	AGAAATTTCAATNGATAGTACTCTCAGAGAGCAGTGAACCCAGACAGATATGTCAAT	721		
Db	26	AGAAATTTCAATNGATAGTACTCTCAGAGAGCAGTGAACCCAGACAGATATGTCAAT	85		
Qy	722	CTGGAGGTCACCGGACTCATGGGTGTTGGTGTATTGACCTCAAGGTGAGACCT	781		
Db	86	CTGGAGGTCACCGGACTCATGGGTGTTGGTGTATTGACCTCAAGGTGAGACACT	145		
Qy	782	GTTGTTCATGAACGTGTAGAGGCTTTGGAAACCTGAAAAGGAAGGTGTGAGACTTGA	841		
Db	146	GTTGTTCATGAATGTATGTATGAGGCTTTGGAAACCTGAAAAGGAAGGTGTGAGACTTGA	205		
Qy	842	AGAACAAATTTGTTGGCAAGCTGGAGATCAGAAAGAAATTTGGCTCTTGTTCTACTAG	901		
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Db	266	TGGGCAGAGGAGATTTCAAGACTCCTTCAAGAGGCGTGGCGGTATATTAAAGCTGAC	325
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LOCUS	BG194269
DEFINITION	BG194269 767 bp mRNA linear EST 21-APR-2001
ACCESSION	R8131313 Atherys RAGE Library Homo sapiens cDNA, mRNA sequence.
VERSION	BG194269
KEYWORDS	GI:13715956
SOURCE	EST.
ORGANISM	Homo sapiens (human)
	Homo sapiens
	Homo sapiens

REFERENCE
AUTHORS

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 767)
Harrington, J. J., Sherf, B., Rundlett, S., Jackson, P. D., Perry, R.,

TITLE
Creation of genome-wide protein expression libraries using random activation of gene expression
Nat. Biotechnol. 19 (5), 440-445 (2001)

MEDLINE 21227151
PUBMED 11329013
COMMENT
Contact: Scott J. Cain
Athersys, Inc.
3201 Carnegie Ave, Cleveland, OH 44115, USA
Tel: 216 431 9900
Fax: 216 361 9896
Email: scain@athersys.com
High quality sequence stop: 550.

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FEATURES
source
location/Qualifiers
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/notes="See 'Creation of Genome-wide Protein Expression
Libraries using Random Activation of Gene Expression',
Nature Biotechnology', in press. Note that even though the
cell type indicated is HT1080, since a random activation
method was used, these sequence tags are not necessarily
expressed in HT1080 under normal circumstances."

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Db 144 GAATTTCACAAATGTGATAGTACTCTCAGAGAGAGAGTGAACACAGACAGATATGTCATTTC 203
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 Qy 1203 GAGCAGCGTATCTAAAAAATTTGGGAAACAAACAATTCAGCGGCTATCCACTGTATACA 1262
 Db 684 GAGCAGCGTATCTAAAAAATTTGGGAAACAAACAATTCAGCGGCTATCCACTGTATACA 743
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RESULT 14
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 LOCUS UI-HF-C80-aca-a-02-0-UI.r1 NIH MGC_210 Homo sapiens cDNA clone
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 ACCESSION CF135099
 VERSION CF135099.1 GI:33250543
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 427)
 Normalization and subtraction: two approaches to facilitate gene discovery
 Genome Res. 6 (9), 791-806 (1996)
 JOURNAL MEDLINE 97044477
 PUBMED 8889548
 COMMENT Contact: Soares, MB
 Coordinated Laboratory for Computational Genomics
 University of Iowa
 375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA
 Tel: 319 335 8250
 Fax: 319 335 9565
 Email: bento-soares@uiowa.edu
 Tissue Procurement: Tim Ratliff
 cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
 DNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clome Distribution: Distribution information can be found at
<http://genome.uiowa.edu/distribution/humanfl.html>
 Seq primer: pYX-5.
 Location/Qualifiers
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 /mol_type="mRNA"
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 /clone="IMAGE:3096075"
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 /notes="Organ: Prostate; Vector: pT73 Pac; Site 1: EcoR I; Site 2: Not I; The library was constructed according to Bonta, Lomon and Soares, Genome Research, 6:791-806, 1996. Denatured RNA was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with oligo-dT primer containing a Not I site. Double strand cDNA was size selected according to mRNA size fraction, ligated with EcoR I adaptor, digested with Not I and then cloned directionally into pT73 Pac vector. The library tag sequence located between the Not I site and the polyA tail is CCCAC. Tissue was provided by Tim Ratliff."

ORIGIN
 Query Match 12.1%; Score 242; DB 14; Length 427;
 Best Local Similarity 99.4%; Pred. No. 2;3e-36;
 Matches 342; Conservative 2; Indels 0; Gaps 0;

Qy 662 AGAATTTCACATGTGATAGTACTCTCAGAGAGAGAGTGAACACAGACAGATATGTCATT 721
 Db 37 AGAATTTCACATGTGATAGTACTCTCAGAGAGAGAGTGAACACAGACAGATATGTCATT 96
 Qy 722 CTGGAGGTCACCGGAGCTCATGGGCTTTGGTGGATATGACCCCTCAGATGGAGACGCT 781
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 Qy 782 GTTGTTCATGAACTGTGAGAGCTTTGGAAACACTGAAAAGAGAGGCTGAGACCTTGA 841
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 Qy 842 AGAACAATTTGTTTGGACCTGGAGATGCAAGAAATTTGGTCTTCTTGGTCTACTGAG 901
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 Qy 902 TGGGAGAGGATTAATTCAGACTCTTCAAGAGCGTGGCGCTTATTAATTAATGCTGAC 961
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RESULT 15
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 ACCESSION CF141546
 VERSION CF141546.1 GI:33256990
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 432)
 Normalization and subtraction: two approaches to facilitate gene discovery
 Genome Res. 6 (9), 791-806 (1996)
 JOURNAL MEDLINE 97044477
 PUBMED 8889548

COMMENT

Contact: Soares, MB
Coordinated Laboratory for Computational Genomics
University of Iowa
375 Newcom Road, 4156 MEBRF, Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: bento-soares@uiowa.edu
Tissue Procurement: Tim Ratliff
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
<http://genome.uiowa.edu/distribution/humanfl.html>
Seq primer: pyx-5.

FEATURES

source

Location/Qualifiers

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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3099613"
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/lab_host="DH10B (TI phage resistant)"
/clone_1lb="NIH_MGC_210"
/note="Organ: Prostate; Vector: pTR73 Pac; Site 1: Ecor I;
Site 2: Not I; The library was constructed according
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with oligo-dT
primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction, ligated
with Ecor I adaptor, digested with Not I and then cloned
directionally into pTR73 Pac vector. The library tag
sequence located between the Not I site and the polyA tail
is CCCAC. Tissue was provided by Tim Ratliff."

ORIGIN

Query Match

11.5%; Score 229; DB 14; Length 432;

Best Local Similarity 99.2%; Pred. No. 6e-34; Indels 0; Gaps 0;

Matches 379; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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QY 552 GCAGCTGGAGAGAGAGCTCAAGTGTCTACAAATGTTGAGCTGGCTTACTGGAAC 611
Db 111 GCAGCTGGAGAGAGAGCTCAAGTGTCTACAAATGTTGAGCTGGCTTACTGGAAC 170
QY 612 TTCTACACAAAAGTCAGATGACATCCACTTACCAATGAAGTACGAGAATTACA 671
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Job time : 3565 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 17, 2004, 16:54:30 ; Search time 115 Seconds
(without alignments)
9612.715 Million cell updates/sec

Title: US-09-973-382C-1

Perfect score: 1992
Sequence: 1 agcaatactactactacaca.....taaaaaaaaaaaaaaaaaa 1992

Scoring table: OLIGO_NNC

Gapop 60.0 , Gapext 60.0

Searched: 682709 seqs, 277475446 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	646	32.4	2133	US-09-164-034B-1	GENERAL INFORMA
2	646	32.4	2653	US-08-325-553-1	Sequence 1, Appl
3	646	32.4	2653	US-08-394-152A-1	Sequence 1, Appl
4	646	32.4	2653	US-08-705-477E-1	Sequence 1, Appl
5	385	19.3	2387	US-08-705-477E-100	Sequence 100, App
6	108	5.4	231	US-09-439-313-454	Sequence 454, App
7	108	5.4	231	US-09-352-616A-454	Sequence 454, App
8	108	5.4	231	US-09-636-215-454	Sequence 454, App
9	108	5.4	231	US-09-685-166A-454	Sequence 454, App
10	59	3.0	782	US-08-705-477E-97	Sequence 97, Appl
11	59	3.0	783	US-08-705-477E-96	Sequence 96, Appl
12	50	2.5	50	US-08-832-468-2	Sequence 2, Appl
13	50	2.5	50	US-08-832-468-6	Sequence 2, Appl
14	38	1.9	893	US-08-394-152A-45	Sequence 45, Appl
15	38	1.9	36	US-08-325-553-32	Sequence 32, Appl
16	29	1.5	36	US-08-325-553-33	Sequence 33, Appl
17	29	1.5	36	US-08-394-152A-32	Sequence 32, Appl
18	29	1.5	36	US-08-394-152A-33	Sequence 33, Appl
19	29	1.5	36	US-08-705-477E-32	Sequence 32, Appl
20	29	1.5	36	US-08-705-477E-33	Sequence 33, Appl
21	29	1.5	54	US-09-493-491-49	Sequence 49, Appl
22	29	1.5	54	US-09-493-491A-49	Sequence 49, Appl
23	26	1.3	309	US-08-171-385-11	Sequence 11, Appl
24	26	1.3	309	US-08-361-441B-11	Sequence 11, Appl
25	26	1.3	911	US-09-461-325-63	Sequence 63, Appl
26	26	1.3	911	US-10-012-542-63	Sequence 63, Appl
27	26	1.3	1412	US-09-644-907B-3	Sequence 3, Appl

C	28	25	1.3	320	1	US-08-171-385-18	Sequence 18, Appl
C	29	25	1.3	320	3	US-08-361-441B-18	Sequence 18, Appl
C	30	25	1.3	951	2	US-09-247-373B-41	Sequence 41, Appl
C	31	25	1.3	1078	2	US-08-555-723B-1	Sequence 1, Appl
C	32	25	1.3	1078	3	US-09-123-465-1	Sequence 1, Appl
C	33	25	1.3	1421	3	US-09-435-019-23	Sequence 23, Appl
C	34	25	1.3	1421	4	US-09-435-019-24	Sequence 24, Appl
C	35	25	1.3	3166	3	US-08-863-102-3	Sequence 3, Appl
C	36	25	1.3	3440	4	US-09-016-434-1489	Sequence 1489, App
C	37	25	1.3	5238	3	US-09-080-855-1	Sequence 1, Appl
C	38	25	1.3	5238	4	US-09-566-076-1	Sequence 1, Appl
C	39	24	1.2	24	4	US-09-493-491-50	Sequence 50, Appl
C	40	24	1.2	24	4	US-09-493-491A-50	Sequence 50, Appl
C	41	24	1.2	24	4	US-08-705-477E-124	Sequence 124, App
C	42	24	1.2	24	4	US-08-705-477E-125	Sequence 125, App
C	43	24	1.2	773	3	US-09-248-335-39	Sequence 35, Appl
C	44	24	1.2	1137	1	US-08-706-214-2	Sequence 2, Appl
C	45	24	1.2	1759	4	US-09-667-135-3	Sequence 3, Appl

ALIGNMENTS

RESULT 1
US-09-164-034B-1
GENERAL INFORMATION:
APPLICANT: Mincheff, Milcho S.
Zoubak, Serguei
TITLE OF INVENTION: Immunotherapy of Cancer Through Expression of Truncated Tumor- or Tumor-Associated Antigen
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: William S. Ramsey,
Ramsey, Cook, Looper & Kurlander, LLC
STREET: 10420 Little Patuxent Parkway, Suite 250
CITY: Columbia
STATE: Maryland
COUNTRY: USA
ZIP: 21044
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MB storage
COMPUTER: PC
OPERATING SYSTEM: Windows 95
SOFTWARE: WordPerfect 8
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/164,034B
FILING DATE: 30-Sep-1998
ATTORNEY/AGENT INFORMATION:
NAME: Ramsey, William S.
REGISTRATION NUMBER: 32,715
REFERENCE/DOCKET NUMBER: b711
TELECOMMUNICATION INFORMATION:
TELEPHONE: (410) 992-9660
TELEFAX: (410) 992-9540
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-164-034B-1
Query Match 32.4%; Score 646; DB 4; Length 2133;
Best Local Similarity 99.2%; Pred. No. 4.3e-271;
Matches 1096; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
Db 607 GGTGGAATCTTCTGAGGTGTGTCACGCGGAAATATCTTAATCGAATGCGCA 666
Qy 335 GGTGGAATCTTCTGAGGTGTGTCACGCGGAAATATCTTAATCGAATGCGCA 394
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Qy 395 GAGACCCCTCTCACACAGGTTACCCAGCAATGATACCTATAGGATGCA 454
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Qy 455 GAGCGTGTGTTCTTCCAGATATCTTCTGTCATCCAGTTGATGATGACAGAG 514
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 DB 1687 AGAAGATGCTGACAAATCTACA 1711

RESULT 2
 US-08-325-553-1
 Sequence 1, Application US/08325553
 Patent No. 553886
 GENERAL INFORMATION:
 APPLICANT: Israeli, Ron S.
 APPLICANT: Heston, Warren D. W.

APPLICANT: Fair, William R.
 TITLE OF INVENTION: THE PROSTATE-SPECIFIC MEMBRANE ANTIGEN
 NUMBER OF SEQUENCES: 38
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Cooper & Dunham
 STREET: 30 Rockefeller Plaza
 CITY: New York
 STATE: New York
 COUNTRY: United States of America
 ZIP: 10112
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/325,553
 FILING DATE:
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/07/973,337A
 FILING DATE: 05 NOV 1992
 ATTORNEY/AGENT INFORMATION:
 NAME: White, John P.
 REGISTRATION NUMBER: 28,678
 REFERENCE/DOCKET NUMBER: 1747/41426
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 977-9550
 TELEFAX: (212) 664-0525
 TELEX: 422523 COOP UI
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2653 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 ORIGINAL SOURCE:
 ORGANISM: Homo sapiens
 TISSUE TYPE: Carcinoma
 IMMEDIATE SOURCE:
 CLONE: Prostate-Specific Membrane Antigen
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 262..2511
 US-08-325-553-1

Query Match 32.4%; Score 646; DB 1; Length 2653;
 Best Local Similarity 99.2%; Pred. No. 4,2e-271;
 Matches 1096; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 335 GGTGGAAATCTTCTGAGAGTGTGTCTCAGCGTGAATAATCTTAATCTGAATGTGCA 394
 DB 994 GGTGGAAATCTTCTGAGAGTGTGTCTCAGCGTGAATAATCTTAATCTGAATGTGCA 1053
 QY 395 GGAAGACCTCTCAGACAGGTTTACCGAGCAATGAATAGCTTATGCGATGGAATTGCA 454
 DB 1054 GGAAGACCTCTCAGACAGGTTTACCGAGCAATGAATAGCTTATGCGGTGGAATTGCA 1113
 QY 455 GAGGCTGTTGGTCTTCCAGATATCTCTGTTCTATCCAGTTGGAATCATATGATGCAAGAG 514
 DB 1114 GAGGCTGTTGGTCTTCCAGATATCTCTGTTCTATCCAGTTGGAATCATATGATGCAAGAG 1173
 QY 515 CTCTAGAAAAAATGGGTGGCTGAGCACCAGATAGCAGCTGGAGGAGTCTCAAA 574
 DB 1174 CTCTAGAAAAAATGGGTGGCTGAGCACCAGATAGCAGCTGGAGGAGTCTCAAA 1233
 QY 575 GTGTCTTACAAATGTGGACCTGGCTTTTCTGAAACTTTTCTACAAAAAGTCAAGATG 634
 DB 1234 GTGTCTTACAAATGTGGACCTGGCTTTTCTGAAACTTTTCTACAAAAAGTCAAGATG 1293

OY	635	CACATCCACTCTAACCAATGAAGTGCACGAAATTTCAATGTGATATGTGATCTCAGAGAA	694
Db	1294	CACATCCACTCTAACCAATGATGTGCAAGAAATTTCAATGTGATATGTGATCTCAGAGAA	1355
OY	695	GCAGTGAACCAAGACAGATATGTCTTCTGAGAGTCAACCGGACTCATGGGTGTTTGGT	754
Db	1354	GCAGTGAACCAAGACAGATATGTCTTCTGAGAGTCAACCGGACTCATGGGTGTTTGGT	1413
OY	755	GGTATTGACCCCTCAGAGTGGAGCGACTGTGTTCATGTGAACCTGTGAGAGAGCTTTGGAA	814
Db	1414	GGTATTGACCCCTCAGAGTGGAGCGACTGTGTTCATGTGAACCTGTGAGAGAGCTTTGGAA	1473
OY	815	CTGAAAAAGGAAGGCTGAGAGACTCTGAGAGAAACAATTTTGTTTGCAAGCTGGGATCGAGA	874
Db	1474	CTGAAAAAGGAAGGCTGAGAGACTCTGAGAGAAACAATTTTGTTTGCAAGCTGGGATCGAGA	1533
OY	875	GAATTTGGTCTTCTTGTTCTACTGAGTGGCGAGAGATTAATTCAGACTCTCTTCAGAG	934
Db	1534	GAATTTGGTCTTCTTGTTCTACTGAGTGGCGAGAGATTAATTCAGACTCTCTTCAGAG	1593
OY	935	CGTGGCGGTCTTATTAATGCTGACCTCATCTATAGAAGGAACTACACTGTGAGATT	994
Db	1594	CGTGGCGGTCTTATTAATGCTGACCTCATCTATAGAAGGAACTACACTGTGAGATT	1653
OY	995	GATTGTACACCACTGATGTAGACGTTGGTATACAACTTAACAAAAGAGCTGAAAAGCCCT	1054
Db	1654	GATTGTACACCGCTGATGTAGACGTTGGTATACAACTTAACAAAAGAGCTGAAAAGCCCT	1713
OY	1055	GATGAAGGCTTTGAAGGCAATCTCTTATAGAAAGTTGAGACTTAAAAAAAGTCCTTCCCA	1114
Db	1714	GATGAAGGCTTTGAAGGCAATCTCTTATAGAAAGTTGAGACTTAAAAAAAGTCCTTCCCA	1773
OY	1115	GAGTTCAGTGCGATGCCCCAGATTAAGCAAAATTTGGACTGTGAAATGATTTTGAGGTGCTC	1174
Db	1774	GAGTTCAGTGCGATGCCCCAGATTAAGCAAAATTTGGACTGTGAAATGATTTTGAGGTGCTC	1833
OY	1175	TTCCAAACGACTTGGAAATTTCTTACGAGCAGAGCAGCGTACTTAAAAATTTGGAAAACAAC	1234
Db	1834	TTCCAAACGACTTGGAAATTTCTTACGAGCAGAGCAGCGTACTTAAAAATTTGGAAAACAAC	1893
OY	1235	AAATTTCAAGCGGCTATCCACTGTATTCACAGTGTCTTGAACAATATGATTTGGTGAAGAAG	1294
Db	1894	AAATTTCAAGCGGCTATCCACTGTATTCACAGTGTCTTGAACAATATGATTTGGTGAAGAAG	1953
OY	1295	TTTTATGATTCAAATGTTTAAATATCACTCACTGTGGGCCAGAGTTCGAGAGAGGATGTGTG	1354
Db	1954	TTTTATGATTCAAATGTTTAAATATCACTCACTGTGGGCCAGAGTTCGAGAGAGGATGTGTG	2013
OY	1355	TTTGAGCTAGCCAAATTCATATAGTGTCCCTTTTGAATGTGCAGAGATTATGCTGTAGTTTAA	1414
Db	2014	TTTGAGCTAGCCAAATTCATATAGTGTCCCTTTTGAATGTGCAGAGATTATGCTGTAGTTTAA	2073
OY	1415	AGAAAGTATGCTGACAAATCTAC	1439
Db	2074	AGAAAGTATGCTGACAAATCTAC	2098

RESULT 3
 US-08-394-152A-1
 Sequence 1, Application US/08394152A
 Patent No. 5935818
 GENERAL INFORMATION:
 APPLICANT: Israeli, Ron S.
 APPLICANT: Heston, Warren D.W.
 APPLICANT: Fair, William R.
 TITLE OF INVENTION: PROSTATE-SPECIFIC MEMBRANE ANTIGEN AND
 TITLE OF INVENTION: US8 THEROP
 NUMBER OF SEQUENCES: 48
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Cooper & Dunham LLP
 STREET: 1185 Avenue of the Americas
 CITY: New York
 STATE: New York

1 COUNTRY: United States of America
2 ZIP: 10036
3
4 COMPUTER READABLE FORM:
5 MEDIUM TYPE: Floppy disk
6 COMPUTER: IBM 330 466 DX2
7 OPERATING SYSTEM: PC-DOS/MS-DOS
8 SOFTWARE: Patent In Release #1.0, Version #1.25
9 CURRENT APPLICATION DATA:
10 APPLICATION NUMBER: US/08/394,152A
11 FILING DATE: 24-FEB-95
12
13 CLASSIFICATION: 435
14 ATTORNEY/AGENT INFORMATION:
15 NAME: White, John P.
16 REGISTRATION NUMBER: 28,678
17 REFERENCE/DOCKET NUMBER: 41426-B
18 TELECOMMUNICATION INFORMATION:
19 TELEPHONE: (212) 278-0400
20 TELEFAX: (212) 391-0525
21 INFORMATION FOR SEQ ID NO: 1:
22 SEQUENCE CHARACTERISTICS:
23 LENGTH: 2553 base pairs
24 TYPE: nucleic acid
25 STRANDEDNESS: double
26 TOPOLOGY: linear
27 MOLECULE TYPE: cDNA
28 HYPOTHEetical: NO
29 ANTI-SENSE: NO
30 ORIGINAL SOURCE:
31 ORGANISM: Homo sapiens
32 TISSUE TYPE: Carcinoma
33 IMMEDIATE SOURCE:
34 CLONE: Prostate-Specific Membrane Antigen
35 FEATURE:
36 NAME/KEY: CDS
37 LOCATION: 262..2511
38
39 US-08-394-152A-1

	Query Match	Similarity	32.4%	Score	646:	DB	2:	Length	2653:
	Best Local	Similarity	99.2%	Pred.	NO.	4.2e-271:			
	Matches	1096:	Conservative	0:	Mismatches	9:	Indels	0:	Gaps
QY	335	GGTTGGAATCTTCTCGAGGTGTGTTCACAGCGTGGAATATATCTTAAATCTGAATGTGCA	394						
Db	994	GGTTGGAATCTTCTCGAGGTGTGTTCACAGCGTGGAATATCTTAAATCTGAATGTGCA	1053						
QY	395	GGAAACCTCTCAACAAGGTTACCCGACAAATGAATATACGCTTATAGCATGGAATTGCA	454						
Db	1054	GGAAACCTCTCAACAAGGTTACCCGACAAATGAATATCTTATAGCGGTGAATTGCA	1113						
QY	455	GAGCGTTGGTCTTCCAGATATTCCTGTTTCATCCAGTTGGATCTATATGATGCACAGAG	514						
Db	1114	GAGCGTTGGTCTTCCAGATATTCCTGTTTCATCCAGTTGGATCTATATGATGCACAGAG	1173						
QY	515	CTCTAGAAAAAATGGGTGGCTCAGACACACAGATATGCACTGAGAGGAAGTCTCAA	574						
Db	1174	CTCTAGAAAAAATGGGTGGCTCAGACACACAGATATGCACTGAGAGGAAGTCTCAA	1233						
QY	575	GTCGTCATCAATGTTGGACCTGCGCTTACTGGAACCTTTCTACACAAAAAGTCAAGATG	634						
Db	1234	GTCGTCATCAATGTTGGACCTGCGCTTACTGGAACCTTTCTACACAAAAAGTCAAGATG	1293						
QY	635	CACATCCACTTCACCAATGAATGAACGAATTTTACATATGTATAGTACTCTCAAGGA	694						
Db	1294	CACATCCACTTCACCAATGAATGAACGAATTTTACATATGTATAGTACTCTCAAGGA	1353						
QY	695	GCAATGGAACCAAGACATATGTTCATCTTGGAGAGTCAACGGGACATAGGGGTGTTGGT	754						
Db	1354	GCAATGGAACCAAGACATATGTTCATCTTGGAGAGTCAACGGGACATAGGGGTGTTGGT	1413						
QY	755	GGTATTGAACCTTCAGATGAGACAGCTGTGTTTCATGAATCTGTGAGGAGCTTTGGAAACA	814						
Db	1414	GGTATTGAACCTTCAGATGAGACAGCTGTGTTTCATGAATCTGTGAGGAGCTTTGGAAACA	1473						

QY 815 CTGAAAAAGGAGGCTGAGACCTAGAGAACATTTTGTTCAGAGCTGGATGACGAA 874
 Db 1474 CTGAAAAAGGAGGCTGAGACCTAGAGAACATTTTGTTCAGAGCTGGATGACGAA 1533
 QY 875 GAATTTGGCTTTCTTGGTTCTTACTGAGTGGGACAGAGATTAATTCAGACTCTTCAAGAG 934
 Db 1534 GAATTTGGCTTTCTTGGTTCTTACTGAGTGGGACAGAGATTAATTCAGACTCTTCAAGAG 1593
 QY 935 CGTGGGCTGGCTTAATTAATTAATGCTGATCTATTAAGAAATCACTGAGAGTT 994
 Db 1594 CGTGGGCTGGCTTAATTAATTAATGCTGATCTATTAAGAAATCACTGAGAGTT 1653
 QY 995 GATTGTACACCACTGATGTACAGCTTGTATACACCTTAACAAAGAGCTGAAAAGCCCT 1054
 Db 1654 GATTGTACACCGCTGATGTACAGCTTGTATACACCTTAACAAAGAGCTGAAAAGCCCT 1713
 QY 1055 GATGAAGGCTTTGAGAGCAATCTCTTATGAAAAGTTGACCTAATAAAAGTCTTCCCA 1114
 Db 1714 GATGAAGGCTTTGAGAGCAATCTCTTATGAAAAGTTGACCTAATAAAAGTCTTCCCA 1773
 QY 1115 GAGTTGAGTGGCAATGCCAGATTAAGCAATGGGATCTGAAAATGATTTTGAAGTGTTC 1174
 Db 1774 GAGTTGAGTGGCAATGCCAGATTAAGCAATGGGATCTGAAAATGATTTTGAAGTGTTC 1833
 QY 1175 TTCCAAAGCACTTGGAAATTTGCTTCAAGCAGACACGCTATATAAAATTTGGAAAACAAAC 1234
 Db 1834 TTCCAAAGCACTTGGAAATTTGCTTCAAGCAGACACGCTATATAAAATTTGGAAAACAAAC 1893
 QY 1235 AAATTCAGCGGCTATCCACTGTATCACAGTGTCTATGAAAACATATGAGTTGGTGAAG 1294
 Db 1894 AAATTCAGCGGCTATCCACTGTATCACAGTGTCTATGAAAACATATGAGTTGGTGAAG 1953
 QY 1295 TTTTATGATCCAAATGTTAAATTAATTAATCACTGACGTGGCCAGAGTTCAGAGAGGATGTG 1354
 Db 1954 TTTTATGATCCAAATGTTAAATTAATTAATCACTGACGTGGCCAGAGTTCAGAGAGGATGTG 2013
 QY 1355 TTTGAGCTAGCCAAATTCATATGATGCTCCCTTTGATTTGAGATTAATGCTGATGTTTA 1414
 Db 2014 TTTGAGCTAGCCAAATTCATATGATGCTCCCTTTGATTTGAGATTAATGCTGATGTTTA 2073
 QY 1415 AGAAGTATGCTGACAAAATCTTACA 1439
 Db 2074 AGAAGTATGCTGACAAAATCTTACA 2098

RESULT 4
 US-08-705-477E-1
 ; Sequence 1, Application US/08705477E
 ; Patent No. 6569432
 ; GENERAL INFORMATION:
 ; APPLICANT: Israeli, Ron S
 ; APPLICANT: Heston, Warren D.W.
 ; APPLICANT: Fair, William R.
 ; APPLICANT: Overfell, Ouathek
 ; APPLICANT: Pinto, John
 ; TITLE OF INVENTION: PROSTATE-SPECIFIC MEMBRANE ANTIGEN AND USES THEREOF
 ; FILE REFERENCE: 1769/41426-G
 ; CURRENT APPLICATION NUMBER: US/08/705,477E
 ; NUMBER OF SEQ ID NOS: 128
 ; SOFTWARE: Patent version 3.1
 ; SEQ ID NO 1
 ; LENGTH: 2653
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; US-08-705-477E-1

Query Match 32.4%; Score 646; DB 4; Length 2653;
 Best local Similarity 99.2%; Pred. No. 4.2e-271;
 Matches 1096; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 335 GGTTGGAATCTTCTGAGAGGTGTGTCAGCGTGAATAATCTTAATCTGAATGTGCA 394
 |||||

Db 994 GGTTGGAATCTTCTGAGAGGTGTGTCAGCGTGAATAATCTTAATCTGAATGTGCA 1053
 QY 395 GGAAGACCCCTCAACACAGTTTACCCAGAAATGAATAGCTTAATAGGATGAATGCA 454
 |||||
 Db 1054 GGAAGACCCCTCAACACAGTTTACCCAGAAATGAATAGCTTAATAGGATGAATGCA 1113
 QY 455 GAGGCTGTTGCTTCCAAAGTATTCCTGTTCAATCCAGTGTGATATGATGACAGAG 514
 Db 1114 GAGGCTGTTGCTTCCAAAGTATTCCTGTTCAATCCAGTGTGATATGATGACAGAG 1173
 QY 515 CTCCTGAAAAAATGGGTGGCTGACCAACAGATAGAGCTGAGAGAGAGTCTCAAA 574
 Db 1174 CTCCTGAAAAAATGGGTGGCTGACCAACAGATAGAGCTGAGAGAGAGTCTCAAA 1233
 QY 575 GGTGCTTAAGTTGGAACGTGGCTTAATGGAACCTTTCTACCAAAAGTCAAGATG 634
 Db 1234 GGTGCTTAAGTTGGAACGTGGCTTAATGGAACCTTTCTACCAAAAGTCAAGATG 1293
 QY 635 CACATCCACTTACCAATGAGTACAGAAATTTACATGTATGATCTCTCAGAGGA 694
 Db 1294 CACATCCACTTACCAATGAGTACAGAAATTTACATGTATGATCTCTCAGAGGA 1353
 QY 695 GCAGTGGAACCAAGACATATGTCAATCTGGAGAGTCAACCGGACTCATGGGTGTTG 754
 Db 1354 GCAGTGGAACCAAGACATATGTCAATCTGGAGAGTCAACCGGACTCATGGGTGTTG 1413
 QY 755 GGATTTAGCCCTCAGAGTGGAGAGCTGTTGTTCAATGAATGTGAGAGCTTTGGACA 814
 Db 1414 GGATTTAGCCCTCAGAGTGGAGAGCTGTTGTTCAATGAATGTGAGAGCTTTGGACA 1473
 QY 815 CTGAAAAAGGAGGCTGAGACCTAGAGAACATTTTGTTCAGAGCTGGATGACGAA 874
 Db 1474 CTGAAAAAGGAGGCTGAGACCTAGAGAACATTTTGTTCAGAGCTGGATGACGAA 1533
 QY 875 GAATTTGGCTTTCTTGGTTCTTACTGAGTGGGACAGAGATTAATTCAGACTCTTCAAGAG 934
 Db 1534 GAATTTGGCTTTCTTGGTTCTTACTGAGTGGGACAGAGATTAATTCAGACTCTTCAAGAG 1593
 QY 935 CGTGGGCTGGCTTAATTAATTAATGCTGATCTATTAAGAAATCACTGAGAGTT 994
 Db 1594 CGTGGGCTGGCTTAATTAATTAATGCTGATCTATTAAGAAATCACTGAGAGTT 1653
 QY 995 GATTGTACACCACTGATGTACAGCTTGTATACACCTTAACAAAGAGCTGAAAAGCCCT 1054
 Db 1654 GATTGTACACCGCTGATGTACAGCTTGTATACACCTTAACAAAGAGCTGAAAAGCCCT 1713
 QY 1055 GATGAAGGCTTTGAGAGCAATCTCTTATGAAAAGTTGACCTAATAAAAGTCTTCCCA 1114
 Db 1714 GATGAAGGCTTTGAGAGCAATCTCTTATGAAAAGTTGACCTAATAAAAGTCTTCCCA 1773
 QY 1115 GAGTTGAGTGGCAATGCCAGATTAAGCAATGGGATCTGAAAATGATTTTGAAGTGTTC 1174
 Db 1774 GAGTTGAGTGGCAATGCCAGATTAAGCAATGGGATCTGAAAATGATTTTGAAGTGTTC 1833
 QY 1175 TTCCAAAGCACTTGGAAATTTGCTTCAAGCAGACACGCTATATAAAATTTGGAAAACAAAC 1234
 Db 1834 TTCCAAAGCACTTGGAAATTTGCTTCAAGCAGACACGCTATATAAAATTTGGAAAACAAAC 1893
 QY 1235 AAATTCAGCGGCTATCCACTGTATCACAGTGTCTATGAAAACATATGAGTTGGTGAAG 1294
 Db 1894 AAATTCAGCGGCTATCCACTGTATCACAGTGTCTATGAAAACATATGAGTTGGTGAAG 1953
 QY 1295 TTTTATGATCCAAATGTTAAATTAATTAATCACTGACGTGGCCAGAGTTCAGAGAGGATGTG 1354
 Db 1954 TTTTATGATCCAAATGTTAAATTAATTAATCACTGACGTGGCCAGAGTTCAGAGAGGATGTG 2013
 QY 1355 TTTGAGCTAGCCAAATTCATATGATGCTCCCTTTGATTTGAGATTAATGCTGATGTTTA 1414
 Db 2014 TTTGAGCTAGCCAAATTCATATGATGCTCCCTTTGATTTGAGATTAATGCTGATGTTTA 2073
 QY 1415 AGAAGTATGCTGACAAAATCTTACA 1439
 Db 2074 AGAAGTATGCTGACAAAATCTTACA 2098

RESULT 5
US-08-705-477E-100
; Sequence 100, Application US/08705477E
; Patent No. 6569432
; GENERAL INFORMATION:
; APPLICANT: Israel, Ron S.
; APPLICANT: Heston, Warren D.W.
; APPLICANT: Fair, William R.
; APPLICANT: Overfelli, Oualtek
; APPLICANT: Pinto, John
; TITLE OF INVENTION: PROSTATE-SPECIFIC MEMBRANE ANTIGEN AND USES THEREOF
; FILE REFERENCE: 1769/41426-G
; CURRENT APPLICATION NUMBER: US/08/705,477E
; CURRENT FILING DATE: 1996-08-29
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: Patent version 3.1
; SEQ ID NO 100
; LENGTH: 2387
; TYPE: DNA
; ORGANISM: Homo sapiens
US-08-705-477E-100

Query Match 19.3%; Score 385; DB 4; Length 2387;
Best Local Similarity 99.1%; Pred. No. 8.9e-158;
Matches 685; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 685 TCTCAGAGGAGCAGTGAACAGATATGTCATTTCTGGAGGTCAACCGGACTCATG 744
DB 1078 TCTCAGAGGAGCAGTGAACAGATATGTCATTTCTGGAGGTCAACCGGACTCATG 1137

QY 745 GGTGTTGGTGTATTTGACCTCAGATGAGCGCTGTTTATGAAACTGAGAG 804
DB 1138 GGTGTTGGTGTATTTGACCTCAGATGAGCGCTGTTTATGAAACTGAGAG 1197

QY 805 CTTTGAACACTGAAAAAGAGGAGTGAAGCTAGAAACAATTTTGTTCAGCTG 864
DB 1198 CTTTGAACACTGAAAAAGAGGAGTGAAGCTAGAAACAATTTTGTTCAGCTG 1257

QY 865 GGATGCAAGAAATTTGCTCTTCTGTTCTACTAGTGGCAGAGATTAATTCAGACT 924
DB 1258 GGATGCAAGAAATTTGCTCTTCTGTTCTACTAGTGGCAGAGATTAATTCAGACT 1317

QY 925 CTTTGAAGACCGTGGCTGTTTATTAATGCTGACTCATCTATGAAGAACTAC 984
DB 1318 CTTTGAAGACCGTGGCTGTTTATTAATGCTGACTCATCTATGAAGAACTAC 1377

QY 985 TCTGAGAGTGTATGTACACACTGATGTACAGCTGTGTATACAACTTAACAAAGAGCT 1044
DB 1378 TCTGAGAGTGTATGTACACACTGATGTACAGCTGTGTATACAACTTAACAAAGAGCT 1437

QY 1045 GAAAGCCCTGATGAGGCTTTGAAGCAAACTCTTTATGAAGTTGAGCTAAAGAAAG 1104
DB 1438 GAAAGCCCTGATGAGGCTTTGAAGCAAACTCTTTATGAAGTTGAGCTAAAGAAAG 1497

QY 1105 TCCCTCCCGAGAGTGTACGAGCCGCAAGATGAAGAAATGGGATCTGGAATGATTT 1164
DB 1498 TCCCTCCCGAGAGTGTACGAGCCGCAAGATGAAGAAATGGGATCTGGAATGATTT 1557

QY 1165 TGAAGTGTCTTCCAGAGACTTGAATTTGCTTCAGGAGAGCAGGTATATAAAATTTG 1224
DB 1558 TGAAGTGTCTTCCAGAGACTTGAATTTGCTTCAGGAGAGCAGGTATATAAAATTTG 1617

QY 1225 GAAACAAACAAATTCAGCGCTATCACTGTATCAAGTCTATGAACATATGAGTT 1284
DB 1618 GAAACAAACAAATTCAGCGCTATCACTGTATCAAGTCTATGAACATATGAGTT 1677

QY 1285 GGTGGAAGAGTTTATGATCAATGTTTAAATATACACTGCTGCGCCAGGTTCCAGG 1344
DB 1678 GGTGGAAGAGTTTATGATCAATGTTTAAATATACACTGCTGCGCCAGGTTCCAGG 1737

QY 1345 AGGATGTGTGAGCTAGCAATTCATTA 1375

DB 1738 AGGATGTGTGAGCTAGCAATTCATTA 1768

RESULT 6
US-09-439-313-454/c
; Sequence 454, Application US/09439313
; Patent No. 6329505
; GENERAL INFORMATION:
; APPLICANT: Xu, Jianshun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang Yugu
; APPLICANT: Reed, Steven G.
; APPLICANT: Kalos, Michael
; APPLICANT: Fanger, Gary
; APPLICANT: Retter, Mark
; APPLICANT: Solk, John
; APPLICANT: Day, Craig
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; FILE REFERENCE: 210121.427C9
; CURRENT APPLICATION NUMBER: US/09/439,313
; CURRENT FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 575
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 454
; LENGTH: 231
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-439-313-454

Query Match 5.4%; Score 108; DB 4; Length 231;
Best Local Similarity 100.0%; Pred. No. 1.7e-37;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 796 TGTGAGAGCTTTGGAACACTGAAAAAGAGGTGAGACCTTAGAAGCAATTTGTT 855
DB 213 TGTGAGAGCTTTGGAACACTGAAAAAGAGGTGAGACCTTAGAAGCAATTTGTT 154

QY 856 TGCAAGCTGGAGTGCAGAAATTTGCTCTTCTGTTCTACTGAGTG 903
DB 153 TGCAAGCTGGAGTGCAGAAATTTGCTCTTCTGTTCTACTGAGTG 106

RESULT 7
US-09-352-616A-454/c
; Sequence 454, Application US/09352616A
; Patent No. 6395278
; GENERAL INFORMATION:
; APPLICANT: Dillon, Davin C.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang, Yugu
; APPLICANT: Xu, Jianshun
; APPLICANT: Mitcham, Jennifer Lynn
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
; FILE REFERENCE: 210121.427C8
; CURRENT APPLICATION NUMBER: US/09/352,616A
; CURRENT FILING DATE: 1999-07-13
; NUMBER OF SEQ ID NOS: 472
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 454
; LENGTH: 231
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-352-616A-454

Query Match 5.4%; Score 108; DB 4; Length 231;
Best Local Similarity 100.0%; Pred. No. 1.7e-37;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	Db	QY	Db
796	213	856	153
TGTGAGGAGCTTTGGAACCTGAAAAAGGAACGGTGGAGACCTTGAGAGAACTTTGTT	TGTGAGGAGCTTTGGAACCTGAAAAAGGAACGGTGGAGACCTGAGAGAACTTTGTT	TGCAGCTGGGATGCAAGAAATTTGTCTTCTTGCTTCTACTGATG	TGCAGCTGGGATGCAAGAAATTTGTCTTCTTGCTTCTACTGATG
855	154	903	106

RESULT 8
US-09-636-215-454/c
; Sequence 454, Application US/09636215
; Patent No. 6620922

```

GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yugu
APPLICANT: Henderson, Robert A.
APPLICANT: Kalos, Michael D.
APPLICANT: Fanger, Gary R.
APPLICANT: Reiter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darrick
APPLICANT: Li, Samuel
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A. W.
APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.42717C17
CURRENT APPLICATION NUMBER: US/09/636,215
CURRENT FILING DATE: 2000-08-10
NUMBER OF SEQ ID NOS: 852
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 454
LENGTH: 231
TYPE: DNA
ORGANISM: Homo sapiens
US-09-636-215-454

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Query Match 5.4%; Score 108; DB 4; Length 231;
Best Local Similarity 100.0%; Pred. No. 1.7e-37;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0.

QY	796	GGTGGAGGAGCTTTGGAAAGCTGAAAAAGAGGAGTGAGACCTGAGAAAGAACATTTTGT	855
Db	213	TGTGAGGAGCTTTGGAAACCTGAAAAAGAGGAGTGAGACCTGAGAAAGAACATTTTGT	154
QY	856	TGCAGCTGGGATGCAGAGAAATTTGTCTTCTTGCTTCTACTGAGTG	903
Db	153	TGCAGCTGGGATGCAGAGAAATTTGTCTTCTTGCTTCTACTGAGTG	106

RESULT 9
US-09-665-168A-44/C
Sequence 453, Application US/09685166A
Patent No. 6630305
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlockee, Susan L.
APPLICANT: Jiang, Yuqin
APPLICANT: Henderson, Robert A.
APPLICANT: Kalos, Michael D.
APPLICANT: Fanger, Gary R.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.

```

APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darrick
APPLICANT: Li, Samuel
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C21
CURRENT APPLICATION NUMBER: US/09/685,166A
CURRENT FILING DATE: 2000-10-10
NUMBER OF SEQ ID NOS: 898
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 454
LENGTH: 231
TYPE: DNA
ORGANISM: Homo sapiens
US-09-685-166A-454

Query Match          5.4%; Score 108; DB 4; Length 231;
Best Local Similarity 100.0%; Pred. No. 1.7e-37;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0,

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Qy	Db	Qy	Db
796	213	856	153
TGGAAGACCTTTGGAAACACTGAAAAAGAAAGGGGAGACCTTGAAGAACAATTTTGT	TGGAAGACCTTTGGAAACACTGAAAAAGAAAGGGGAGACCTTGAAGAACAATTTTGT	TGCAAGCTGGGATGCAGAAAGAAATTTGGTCTTCTTGGTCTACCTGAGG	TGCAAGCTGGGATGCAGAAAGAAATTTGGTCTTCTTGGTCTACCTGAGG
855	154	903	106
TTTGT	TTTGT	TTTGT	TTTGT

```

RESULT 10
US-08-705-477E-97/C
; Sequence 97, Application US/08705477E
; Patent No. 6569432
; GENERAL INFORMATION:
; APPLICANT: Israeli, Ron S
; APPLICANT: Heston, Warren D.W.
; APPLICANT: Fair, William R.
; APPLICANT: Overfelli, Quatek
; APPLICANT: Pinto, John
; TITLE OF INVENTION: PROSTATE-SPECIFIC MEMBRANE ANTIGEN AND USES THEREOF
; FILE REFERENCE: 1769/41426-G
; CURRENT APPLICATION NUMBER: US/08/705,477E
; CURRENT FILING DATE: 1996-08-29
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 97
; LENGTH: 782
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (505)..(505)
; OTHER INFORMATION: n=any nucleotide
US-08-705-477E-97

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Query Match          3.0%: Score 59; DB 4; Length 782;
Best Local Similarity 100.0%: Pred. NO. 3.2e-16;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0

Oy      36  AATCTGATGTTCTGAGGATTTTATAGACTTATAGTACCAAAAAGAAAGGGAATTCCT 94
        |||||
Db       204 AAATCTGATGTTCTGAGGATTTTATAGACTTATAGTACCAAAAAGAAAGGGAATTCCT 146

RESULT 11
US-08-705-477E--96
; Sequence 96, Application US/08705477E
; Patent No.6569432
; GENERAL INFORMATION:
; APPLICANT: Israeli, Ron S

```

APPLICANT: Heston, Warren D.W.
APPLICANT: Fair, William R.
APPLICANT: Overfelli, Onathek
APPLICANT: Pinto, John
TITLE OF INVENTION: PROSTATE-SPECIFIC MEMBRANE ANTIGEN AND USES THEREOF
FILE REFERENCE: 1169/41426-G
CURRENT FILING DATE: 1996-08-29
NUMBER OF SEQ ID NOS: 128
SOFTWARE: Patent version 3.1
SEQ ID NO 96
LENGTH: 783
TYPE: DNA
ORGANISM: Homo sapiens
US-08-705-477E-96

Query Match 3.0%; Score 59; DB 4; Length 783;
Best Local Similarity 100.0%; Pred. No. 3.2e-16;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 36 AAATCTATGTTCTGAGATTCTTGAAGCTTATAGTACCAAGGAAAGGAAATCT 94
Db 580 AAATCTATGTTCTGAGATTCTTGAAGCTTATAGTACCAAGGAAAGGAAATCT 638

RESULT 12

US-08-832-468-2
Sequence 2, Application US/08832468
Patent No. 5962237

GENERAL INFORMATION:

APPLICANT: Ts'o, Paul O.P.
APPLICANT: Wang, Zheng-Pin
APPLICANT: Lesko, Stephen A.
APPLICANT: Nelson, William G.
APPLICANT: Partin, Alan W.
TITLE OF INVENTION: A METHOD OF ENRICHING RARE CELLS
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Leydig, Volt & Mayer, Ltd.
STREET: 700 Thirteenth St., NW
CITY: Washington
STATE: DC
COUNTRY: US
ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/832,468
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60-014929
FILING DATE: 05-APR-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Jay, Jeremy M.
REGISTRATION NUMBER: 33587
REFERENCE/DOCKET NUMBER: 72466
TELEPHONE: 202-737-6770
TELEFAX: 202-737-6770
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 50 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid (synthetic DNA)
US-08-832-468-2

Query Match 2.5%; Score 50; DB 2; Length 50;
Best Local Similarity 100.0%; Pred. No. 2.7e-12;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1262 AGTGTATGAACATATGATGTTGCGAAGGTTTATGATCATGTT 1311
Db 1 AGTGTATGAACATATGATGTTGCGAAGGTTTATGATCATGTT 50

RESULT 13

US-08-832-468-6
Sequence 6, Application US/08832468
Patent No. 5962237

GENERAL INFORMATION:

APPLICANT: Ts'o, Paul O.P.
APPLICANT: Wang, Zheng-Pin
APPLICANT: Lesko, Stephen A.
APPLICANT: Nelson, William G.
APPLICANT: Partin, Alan W.
TITLE OF INVENTION: A METHOD OF ENRICHING RARE CELLS
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Leydig, Volt & Mayer, Ltd.
STREET: 700 Thirteenth St., NW
CITY: Washington
STATE: DC
COUNTRY: US
ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/832,468
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60-014929
FILING DATE: 05-APR-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Jay, Jeremy M.
REGISTRATION NUMBER: 33587
REFERENCE/DOCKET NUMBER: 72466
TELEPHONE: 202-737-6770
TELEFAX: 202-737-6770
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 50 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid (synthetic DNA)
US-08-832-468-6

Query Match 2.5%; Score 50; DB 2; Length 50;
Best Local Similarity 100.0%; Pred. No. 2.7e-12;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1352 GTGTTGAGCTAGCCCAATTCATAGTGCCTTTGATGTTGAGATTA 1401
Db 1 GTGTTGAGCTAGCCCAATTCATAGTGCCTTTGATGTTGAGATTA 50

RESULT 14

US-08-394-152A-45/C
Sequence 45, Application US/08394152A
Patent No. 5935818

GENERAL INFORMATION:

APPLICANT: Israeli, Ron S.
APPLICANT: Heston, Warren D.W.

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? APPLICANT: Fair, William R.
? TITLE OF INVENTION: PROSTATE-SPECIFIC MEMBRANE ANTIGEN AND
? TITLE OF INVENTION: USES THEREOF
? NUMBER OF SEQUENCES: 48
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: Cooper & Dunham LLP
? STREET: 1185 Avenue of the Americas
? CITY: New York
? STATE: New York
? COUNTRY: United States of America
? ZIP: 10036
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM 330 466 DX2
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: Patentin Release #1.0, Version #1.25
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/394,152A
? FILING DATE: 24-FEB-95
? CLASSIFICATION: 435
? ATTORNEY/AGENT INFORMATION:
? NAME: White, John P.
? REGISTRATION NUMBER: 28,678
? REFERENCE/DOCKET NUMBER: 41426-B
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (212) 278-0400
? TELEFAX: (212) 391-0525
? INFORMATION FOR SEQ ID NO: 45:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 893 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: double
? TOPOLOGY: linear
? MOLECULE TYPE: peptide
? HYPOTHETICAL: NO
? ANTI-SENSE: NO
? ORIGINAL SOURCE:
? ORGANISM: Homo Sapien
? TISSUE TYPE: Carcinoma
? IMMEDIATE SOURCE:
? CLONE: Prostate Specific Membrane Antigen
? US-08-394-152A-45

Query Match 1.9%; Score 38; DB 2; Length 893;
Best Local Similarity 100.0%; Pred. No. 4.2e-07;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 238 CTAGGTTAAATAATGCCAGCTGGCAGGGCCAAAGGAG 275
DB 38 CTAGGTTAAATAATGCCAGCTGGCAGGGCCAAAGGAG 1

RESULT 15
US-08-325-553-32/c
? Sequence 32, Application US/08325553
? Patent No. 5538866
? GENERAL INFORMATION:
? APPLICANT: Israel, Ron S.
? APPLICANT: Heaton, Warren D.W.
? APPLICANT: Fair, William R.
? TITLE OF INVENTION: THE PROSTATE-SPECIFIC MEMBRANE ANTIGEN
? NUMBER OF SEQUENCES: 38
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: Cooper & Dunham
? STREET: 30 Rockefeller Plaza
? CITY: New York
? STATE: New York
? COUNTRY: United States of America
? ZIP: 10112
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
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? SOFTWARE: Patentin Release #1.0, Version #1.25
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/325,553
? FILING DATE:
? CLASSIFICATION: 435
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US/07/973,337A
? FILING DATE: 05 NOV 1992
? ATTORNEY/AGENT INFORMATION:
? NAME: White, John P.
? REGISTRATION NUMBER: 28,678
? REFERENCE/DOCKET NUMBER: 1747/41426
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (212) 977-9550
? TELEFAX: (212) 664-0525
? TELEX: 422523 COOP UT
? INFORMATION FOR SEQ ID NO: 32:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 36 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: double
? TOPOLOGY: linear
? MOLECULE TYPE: peptide
? HYPOTHETICAL: NO
? ANTI-SENSE: NO
? ORIGINAL SOURCE:
? ORGANISM: Homo Sapien
? TISSUE TYPE: Carcinoma
? IMMEDIATE SOURCE:
? CLONE: Prostate Specific Membrane Antigen
? US-08-325-553-32

Query Match 1.5%; Score 29; DB 1; Length 36;
Best Local Similarity 100.0%; Pred. No. 0.0036;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 842 AGAACATTTTGTTCAGAGCTGGGATGC 870
DB 36 AGAACATTTTGTTCAGAGCTGGGATGC 8
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Search completed: February 17, 2004, 19:39:25
Job time : 119 secs